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                  GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:      April 18, 2006, 13:41:26 ; Search time 27 Seconds
                                           (without alignments)
                                        184.120 Million cell updates/sec

Title:       US-10-764-140-4
Perfect score: 617
Sequence:    1 EIQLQQSGPELVKPGASVQV.........RDVTTALDFWGQGTTLTVSS 117

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters:      217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Published Applications AA_New:*
            1: /SIDS57/ptcodata/2/pubpaa/US08_NEW_PUB.pep:*
            2: /SIDS5/ptcodata/2/pubpaa/US06_NEW_PUB.pep:*
            3: /SIDS5/ptcodata/2/pubpaa/US07_NEW_PUB.pep:*
            4: /SIDS5/ptcodata/2/pubpaa/PCT_NEW_PUB.pep:*
            5: /SIDS5/ptcodata/2/pubpaa/US05_NEW_PUB.pep:*
            6: /SIDS5/ptcodata/2/pubpaa/US10_NEW_PUB.pep:*
            7: /SIDS5/ptcodata/2/pubpaa/US11_NEW_PUB.pep:*
            8: /SIDS5/ptcodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	617	100.0	117	7	US-11-087-528-4	Sequence 4, Appli
2	617	100.0	117	7	US-11-122-622-4	Sequence 4, Appli
3	503.5	81.6	137	7	US-11-074-173-39	Sequence 39, Appl
4	498.5	80.8	120	7	US-11-037-199-5	Sequence 5, Appli
5	483	78.3	112	6	US-10-246-019A-6	Sequence 28, Appli
6	468.5	75.9	139	6	US-10-504-389A-6	Sequence 6, Appli
7	466	75.5	118	7	US-11-171-567-203	Sequence 203, App
8	459	74.4	119	7	US-11-097-812-72	Sequence 72, Appl
9	459	74.4	119	7	US-11-097-812-81	Sequence 81, Appl
10	458	74.2	115	7	US-11-165-023-16	Sequence 16, Appl
11	454	73.6	119	7	US-11-097-812-63	Sequence 63, Appl
12	454	73.6	119	7	US-11-097-812-64	Sequence 64, Appl
13	454	73.6	119	7	US-11-097-812-65	Sequence 65, Appl
14	454	73.6	119	7	US-11-097-812-66	Sequence 66, Appl
15	454	73.6	119	7	US-11-097-812-67	Sequence 67, Appl
16	454	73.6	119	7	US-11-097-812-70	Sequence 70, Appl
17	454	73.6	119	7	US-11-097-812-71	Sequence 71, Appl
18	454	73.6	119	7	US-11-097-812-73	Sequence 73, Appl
19	454	73.6	119	7	US-11-097-812-74	Sequence 74, Appl
20	454	73.6	119	7	US-11-097-812-75	Sequence 75, Appl
21	454	73.6	119	7	US-11-097-812-76	Sequence 76, Appl
22	454	73.6	119	7	US-11-097-812-77	Sequence 77, Appl
23	454	73.6	119	7	US-11-097-812-80	Sequence 80, App
24	454	73.6	119	7	US-11-097-812-206	Sequence 206, App
25	454	73.6	120	7	US-11-097-812-136	Sequence 136, App
26	454	73.6	120	7	US-11-097-812-144	Sequence 144, App
27	454	73.6	120	7	US-11-097-812-145	Sequence 145, App
28	454	73.6	122	7	US-11-171-567-204	Sequence 204, App
29	454	73.6	130	7	US-11-188-187A-3	Sequence 3, Appli
30	450.5	73.0	130	7	US-11-179-820-6	Sequence 6, Appli
31	450	72.9	115	7	US-11-165-023-31	Sequence 31, Appl
32	450	72.9	119	7	US-11-097-812-78	Sequence 78, Appl
33	447	72.4	115	7	US-11-165-023-32	Sequence 32, Appl
34	447	72.4	120	7	US-11-097-812-138	Sequence 138, App
35	447	72.4	120	7	US-11-097-812-143	Sequence 143, App
36	445.5	72.2	671	7	US-11-202-507A-14	Sequence 14, Appl
37	445.5	72.2	672	7	US-11-202-507A-7	Sequence 7, Appli
38	444.5	72.0	243	6	US-10-016-686-1	Sequence 1, Appli
39	444.5	72.0	488	6	US-10-016-686-3	Sequence 3, Appli
40	444.5	72.0	592	6	US-10-016-686-4	Sequence 4, Appli
41	444.5	72.0	671	7	US-11-202-507A-8	Sequence 8, Appli
42	444.5	72.0	672	7	US-11-202-507A-6	Sequence 6, Appli
43	443	71.8	120	7	US-11-097-812-135	Sequence 135, App
44	441	71.5	115	7	US-11-218-813-19	Sequence 19, Appl
45	441	71.5	119	6	US-10-507-662-22	Sequence 22, Appl

ALIGNMENTS

```
RESULT 1
US-11-087-528-4
; Sequence 4, Application US/11087528
; Publication No. US20050271664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: WEN, JING HAI
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION:    OF USE THEREOF
; FILE REFERENCE: TNA-005.06
; CURRENT APPLICATION NUMBER: US/11/087,528
; CURRENT FILING DATE: 2005-03-22
; PRIOR APPLICATION NUMBER: 10/293,417
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-087-528-4

Query Match             100.0%;  Score 617;  DB 7;  Length 117;
Best Local Similarity   99.1%;  Pred. No. 5.9e-50;
Matches 116;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db      1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy     61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 2
US-11-122-622-4
; Sequence 4, Application US/11122622
; Publication No. US2006003901A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
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; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/11/122,622
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US/09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-122-622-4

Query Match   100.0%;   Score 617; DB 7; Length 117;
Best Local Similarity   99.1%;   Pred. No. 5.9e-50;
Matches 116; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   1 EIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVFCARDVTTALDFWGQGTTLTVSS 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVFCARDVTTALDFWGQGTTLTVSS 117

RESULT 3
US-11-074-373-39
; Sequence 39, Application US/11074373
; Publication No. US2006024302A1
; GENERAL INFORMATION:
; APPLICANT: Achen et al.
; TITLE OF INVENTION: CHIMERIC ANTI-VEGF-D ANTIBODIES AND HUMANIZED ANTI-VEGF-D ANTIBOD
; TITLE OF INVENTION: AND METHODS OF USING SAME
; FILE REFERENCE: 28967/39969A
; CURRENT APPLICATION NUMBER: US/11/074,373
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-074-373-39

Query Match   81.6%;   Score 503.5; DB 7; Length 137;
Best Local Similarity   78.8%;   Pred. No. 1.8e-39;
Matches   93; Conservative 13; Mismatches 11; Indels   1; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              |||||||||||||||||||| ||:|||||||||||||||||||||||||||||||| |
Db   20 EIQLQQSGPDLVKPGASVKVSCRASGYSFTGYNMYWVKQSHGKSLEWIGYIDPYNGDTTY 79

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVFCAR-DVTTALDFWGQGTTLTVSS 117
              :|||||||||||||||| ||||||||||||||||||| :|||||||||||||||||
Db   80 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARTSYYGGMDYWGQGTSVTVSS 137

RESULT 4
US-11-037-199-5
; Sequence 5, Application US/11037199
; Publication No. US2006003001 5A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: Novel methods of producing antibody-enzyme, the antibody-enzymes,
; TITLE OF INVENTION: and the use thereof
; FILE REFERENCE: A251-01/PCT
; CURRENT APPLICATION NUMBER: US/11/037,199
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: JP 2002-211756

; PRIOR FILING DATE: 2002-7-19
; PRIOR APPLICATION NUMBER: JP 2002-211768
; PRIOR FILING DATE: 2002-7-19
; PRIOR APPLICATION NUMBER: JP 2003-051943
; PRIOR FILING DATE: 2003-2-27
; PRIOR APPLICATION NUMBER: JP 2003-198270
; PRIOR FILING DATE: 2003-7-17
; PRIOR APPLICATION NUMBER: JP 2003-198281
; PRIOR FILING DATE: 2003-7-17
; PRIOR APPLICATION NUMBER: JP 2003-198292
; PRIOR FILING DATE: 2003-7-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-037-199-5

Query Match   80.8%;   Score 498.5; DB 7; Length 120;
Best Local Similarity   79.2%;   Pred. No. 4.4e-39;
Matches   95; Conservative 11; Mismatches 11; Indels   3; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              |||||||||||||||||||||||| |:|||||||||||||||||||||||||||||| |
Db   1 EIQLQQSGPELVRPGASVKVSCKASGYSFTNSIMYWVRQSHGKSLEWIGYIDPYNGGTSY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVFCAR---DVTTALDFWGQGTTLTVSS 117
              :| |||||||||||||:||||||||||||:||||||| :|:||||||||||:|||
Db   61 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYFCARFIVVADVMDYWGQGTSVTVSS 120

RESULT 5
US-10-246-019A-6
; Sequence 6, Application US/10246019A
; Publication No. US2006007313A1
; GENERAL INFORMATION:
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Abrahmson, Julie
; TITLE OF INVENTION: Sialoadhesin Factor-3 Antibodies
; FILE REFERENCE: GH50019-1C1
; CURRENT APPLICATION NUMBER: US/10/246,019A
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: USSN 09/577,930
; PRIOR FILING DATE: 2000-01-22
; PRIOR APPLICATION NUMBER: USSN 09/046,736
; PRIOR FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: USSN 60/041,885
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Human
US-10-246-019A-6

Query Match   78.3%;   Score 483; DB 6; Length 112;
Best Local Similarity   78.4%;   Pred. No. 1.1e-37;
Matches   91; Conservative 10; Mismatches 11; Indels   4; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              :|||||||||||||||||||| ||:|||||||||||||||||||||||||||||| |
Db   1 QIQLQQSGPELVKPGASVKVSCKASGYSFTDYNIYWVKQSHGKSLEWIGYIDPYNDDTGY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVFCARDVTTALDFWGQGTTLTVSS 116
              :|| |||||||||||:||||||||||||:||||||: |||:
Db   61 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCASEGI---HWGQGTLVTVS 112

RESULT 6
US-10-504-389A-28
; Sequence 28, Application US/10504389A

; Publication No. US20060045876A1
; GENERAL INFORMATION:
; APPLICANT: Renner, Christoph
; APPLICANT: Scott, Andrew
; TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
; TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
; FILE REFERENCE: LUD 5821
; CURRENT APPLICATION NUMBER: US/10/504,389A
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: PCT/US03/04243
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 28
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region
US-10-504-389A-28

  Query Match   75.9%;   Score 468.5;   DB 6;   Length 139;
  Best Local Similarity   73.7%;   Pred. No. 2.9e-36;
  Matches   87; Conservative   15; Mismatches   15; Indels   1; Gaps   1;

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Qy      1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
            |:||||||||||||||||||| :||:|||||||||||||:||||||||||||||
Db     18 EVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSHGKSLDWIGYIAPYSGGTGY 77

Qy     61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCA-RDVTTALDFWGQGTTLTVSS 117
            |:||||||||||||||||||||:|||||  |:||||||||||||||||
Db     78 NQEFKNRATLTVDKSSTAYMELRSLTSDDSAVYYCARRDRFPYFDYWGQGTTLRVSS 135
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RESULT 7
US-11-171-567-203
; Sequence 203, Application US/11171567
; Publication No. US20060057551A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC LEUK
; TITLE OF INVENTION: CELLS AND USES THEREOF
; FILE REFERENCE: ALEX-P06-060
; CURRENT APPLICATION NUMBER: US/11/171,567
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US 10/996,316
; PRIOR FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 203
; LENGTH: 118
; TYPE: PRT
; ORGANISM: murine
US-11-171-567-203

  Query Match   75.5%;   Score 466;   DB 7;   Length 118;
  Best Local Similarity   72.6%;   Pred. No. 4.2e-36;
  Matches   85; Conservative   15; Mismatches   17; Indels   0; Gaps   0;

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Qy      1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
            |:||||||||||||||||:::||| ||||||||||||||||||||:|:|||| :|
Db      2 EVQQQQSGPELVKPGASLKMSCKASGYSFTDYIILWVKQNHGKSLEWIGHIDPYYGSSNY 61
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Qy     61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
            |:|||||||||||||:||||||||||||:| | |
Db     62 NLKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCGRSKRDYFDYWGQGTTLTVSS 118
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RESULT 8
US-11-097-812-72
; Sequence 72, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-72

  Query Match   74.4%;   Score 459;   DB 7;   Length 119;
  Best Local Similarity   72.3%;   Pred. No. 1.8e-35;
  Matches   86; Conservative   16; Mismatches   15; Indels   2; Gaps   1;

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Qy      1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
            |:|||||||||| |:||||:|||:|||||| |  ||:||||||||||||||::|
Db      1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSNGKSLEWIGNIDPYYGGTSY 60

Qy     61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVT--TALDFWGQGTTLTVSS 117
            :||||||||||||||||||||||:|:||||||| :|:|||||::||||
Db     61 NQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARTATALSTMDYWGQGTSVTVSS 119
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RESULT 9
US-11-097-812-81
; Sequence 81, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207

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;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 81
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-81

Query Match             74.4%;  Score 459;  DB 7;  Length 119;
Best Local Similarity   72.3%;  Pred. No. 1.8e-35;
Matches   86;  Conservative  16;  Mismatches  15;  Indels   2;  Gaps   1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
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Db          1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMWVKQSNGKSLEWIGNIDPYYGGTSY 60

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVT--TALDFWGQGTTLTVSS 117
              :| |||||||||:||:| | ||||||||||||||||  :  :|:|||||::||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCARTATALSTMDYWGQGTSVTVSS 119

RESULT 10
US-11-165-023-16
;   Sequence 16, Application US/11165,023
;   Publication No. US20060019342A1
;   GENERAL INFORMATION:
;   APPLICANT: Dall'Acqua, William
;   APPLICANT: Wu, Herren
;   APPLICANT: Damschroder, Melissa
;   TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAMMALIAN
;   TITLE OF INVENTION: CELLS BY SITE-DIRECTED MUTAGENESIS
;   FILE REFERENCE: AE700US
;   CURRENT APPLICATION NUMBER: US/11/165,023
;   CURRENT FILING DATE: 2005-06-24
;   PRIOR APPLICATION NUMBER: US 60/583,184
;   PRIOR FILING DATE: 2004-06-25
;   PRIOR APPLICATION NUMBER: US 60/624,153
;   PRIOR FILING DATE: 2004-11-02
;   NUMBER OF SEQ ID NOS: 32
;   SOFTWARE: PatentIn version 3.3
;   SEQ ID NO 16
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: recombinant antibody variable region
US-11-165-023-16

Query Match             74.2%;  Score 458;  DB 7;  Length 115;
Best Local Similarity   71.8%;  Pred. No. 2.2e-35;
Matches   84;  Conservative  17;  Mismatches  14;  Indels   2;  Gaps   1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              |:|||||||||| |||||||   ::||||||||||||||||||| ||:|
Db          1 EVQLQQSGPELVKTGASVKISCKASGYSFTGYMHWVKQSHGKSLEWIGYISCNGVTSY 60

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              :| |||||||||:||:| | ||||||||||||||  : :|:|||||||::|||
Db         61 NQKFKGKATFTVDTSSSTAYMQFNSLTSEDSAVYYCAR--SHAMDYWGQGTSVTVSS 115

RESULT 11
US-11-097-812-63
;   Sequence 63, Application US/11097812
;   Publication No. US2005028182BA1
;   GENERAL INFORMATION:
;   APPLICANT: Bowdish, Katherine S.
;   APPLICANT: Kretz-Rommel, Anke
;   APPLICANT: Dakappagari, Naveen
;   TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;   TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;   FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;   CURRENT APPLICATION NUMBER: US/11/097,812
;   CURRENT FILING DATE: 2005-04-01
```

```
;   PRIOR APPLICATION NUMBER: US 11/016,647
;   PRIOR FILING DATE: 2004-12-17
;   PRIOR APPLICATION NUMBER: PCT/US04/06570
;   PRIOR FILING DATE: 2004-03-04
;   PRIOR APPLICATION NUMBER: US 60/548,385
;   PRIOR FILING DATE: 2004-02-28
;   PRIOR APPLICATION NUMBER: US 60/529,500
;   PRIOR FILING DATE: 2003-12-15
;   PRIOR APPLICATION NUMBER: US 60/451,816
;   PRIOR FILING DATE: 2003-03-04
;   NUMBER OF SEQ ID NOS: 207
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 63
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-63

Query Match             73.6%;  Score 454;  DB 7;  Length 119;
Best Local Similarity   71.4%;  Pred. No. 5.3e-35;
Matches   85;  Conservative  15;  Mismatches  17;  Indels   2;  Gaps   1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              |:|||||||||| |||||||   ||:||||||||||||||||||| |||| ||||
Db          1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMWVKQSNGKSLEWIGNIDPYYGDITY 60

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVT--ALDFWGQGTTLTVSS 117
              :| |||||||||:||:| | |||||||||||||:|||  :  ||:|||||::||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCARTATALYTMDYWGQGTSVTVSS 119

RESULT 12
US-11-097-812-64
;   Sequence 64, Application US/11097812
;   Publication No. US2005028182BA1
;   GENERAL INFORMATION:
;   APPLICANT: Bowdish, Katherine S.
;   APPLICANT: Kretz-Rommel, Anke
;   APPLICANT: Dakappagari, Naveen
;   TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;   TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;   FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;   CURRENT APPLICATION NUMBER: US/11/097,812
;   CURRENT FILING DATE: 2005-04-01
;   PRIOR APPLICATION NUMBER: US 11/016,647
;   PRIOR FILING DATE: 2004-12-17
;   PRIOR APPLICATION NUMBER: PCT/US04/06570
;   PRIOR FILING DATE: 2004-03-04
;   PRIOR APPLICATION NUMBER: US 60/548,385
;   PRIOR FILING DATE: 2004-02-28
;   PRIOR APPLICATION NUMBER: US 60/529,500
;   PRIOR FILING DATE: 2003-12-15
;   PRIOR APPLICATION NUMBER: US 60/451,816
;   PRIOR FILING DATE: 2003-03-04
;   NUMBER OF SEQ ID NOS: 207
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 64
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-64

Query Match             73.6%;  Score 454;  DB 7;  Length 119;
Best Local Similarity   71.4%;  Pred. No. 5.3e-35;
Matches   85;  Conservative  15;  Mismatches  17;  Indels   2;  Gaps   1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
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Db          1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMWVKQSNGKSLEWIGNIDPYYGDITY 60

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVT--ALDFWGQGTTLTVSS 117
              :| |||||||||:||:| | |||||||||||||:|||  :  ||:|||||::||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCARTATALYTMDYWGQGTSVTVSS 119
```

RESULT 13
US-11-097-812-65
; Sequence 65, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-65

Query Match   73.6%; Score 454; DB 7; Length 119;
Best Local Similarity   71.4%; Pred. No. 5.3e-35;
Matches   85; Conservative   15; Mismatches   17; Indels   2; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              : |||||||| ||||||| ||:||||::||||| ||||| |: || |||||||: || :|
Db   1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSNGKSLEWIGNIDPYYGDITY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTT--ALDFWGQGTTLTVSS 117
              : ||||||||||||||:|| ||:||:|||:||||||||:|| :|||||||||::|||
Db   61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCARTATALYTMDYWGQGTSVTVSS 119

RESULT 14
US-11-097-812-66
; Sequence 66, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-66

Query Match   73.6%; Score 454; DB 7; Length 119;
Best Local Similarity   70.6%; Pred. No. 5.3e-35;
Matches   84; Conservative   15; Mismatches   18; Indels   2; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              : |||||||| ||||||| |||:||::||||| ||||| |: || |||||||: ::
Db   1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSSGKSLEWIGNFDPYYGVITY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTT--ALDFWGQGTTLTVSS 117
              : ||||||||||||||:| ||:||:|||||||||||:|| :|||||||||::|||
Db   61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCARTATALYTMDYWGQGTSVTVSS 119

RESULT 15
US-11-097-812-67
; Sequence 67, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 119
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-67

Query Match   73.6%; Score 454; DB 7; Length 119;
Best Local Similarity   70.6%; Pred. No. 5.3e-35;
Matches   84; Conservative   15; Mismatches   18; Indels   2; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              : |||||||| ||||||| |||:||::||||| ||||| |: || |||||||: ::
Db   1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSSGKSLEWIGNFDPYYGVITY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTT--ALDFWGQGTTLTVSS 117
              : ||||||||||||||:| ||:||:||||||||||:|| :|||||||||::|||
Db   61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCARTATALYTMDYWGQGTSVTVSS 119

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Job time : 27 secs

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                    GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:    April 18, 2006, 13:32:05 ; Search time 188 Seconds
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Title:          US-10-764-140-4
Perfect score:  617
Sequence:       1 EIQLQQSGPELVKPGASVQV.........RDVTTALDFWGQGTTLTVSS 117

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:    2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
          1: geneseqp1980s:*
          2: geneseqp1990s:*
          3: geneseqp2000s:*
          4: geneseqp2001s:*
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          6: geneseqp2003as:*
          7: geneseqp2003bs:*
          8: geneseqp2004s:*
          9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	617	100.0	117	2	AAW71288	Aaw71288 Human ant
2	617	100.0	117	6	ABR42700	Abr42700 Anti-tiss
3	617	100.0	117	6	ABR42718	Abr42718 Anti-tiss
4	616	99.8	117	8	ADL35005	Adl35005 Murine an
5	616	99.8	117	8	ADU06810	Adu06810 Murine H3
6	616	99.8	117	9	ADW07328	Adw07328 Mouse ant
7	616	99.8	117	6	ADZ40939	Adz40939 H36.D2.B7
8	611	99.0	117	6	ABR42719	Abr42719 Anti-tiss
9	597	96.8	117	6	ABR42720	Abr42720 Anti-tiss
10	584	94.7	117	6	ABR42721	Abr42721 Anti-tiss
11	571	92.5	117	6	ABR42722	Abr42722 Anti-tiss
12	561	90.9	117	6	ABR42723	Abr42723 Anti-tiss
13	545	88.3	117	6	ABR42730	Abr42730 Anti-tiss
14	542	87.8	117	6	ABR42731	Abr42731 Anti-tiss
15	540	87.5	117	6	ABR42724	Abr42724 Anti-tiss
16	539	87.4	117	6	ABR42729	Abr42729 Anti-tiss
17	536	86.9	117	6	ABR42725	Abr42725 Anti-tiss
18	536	86.9	117	6	ABR42728	Abr42728 Anti-tiss
19	527	85.4	117	6	ABR42726	Abr42726 Anti-tiss
20	521.5	84.5	118	2	AAY52755	Aay52755 Anti-tiss
21	521.5	84.5	118	6	AAY52756	Aay52756 Anti-tiss
22	521	84.4	117	6	ABR42727	Abr42727 Anti-tiss
23	511.5	82.9	120	7	ABR82930	Abr82930 Anti-huma
24	498.5	80.8	120	8	ADI26469	Adi26469 Murine I4
25	493	79.9	117	2	AAW84093	Murine vi
26	492	79.7	119	8	ADR73588	Anti-AR a
27	492	79.7	138	8	ADR73595	Anti-AR a
28	487	78.9	113	3	AAY44588	Mouse ant
29	487	78.9	137	3	AAY44600	Mouse hea
30	487	78.9	236	9	ADW95680	Mouse ant
31	487	78.9	236	9	ADX15685	Mouse ant
32	487	78.9	237	3	AAY44595	EscFv#125
33	487	78.9	243	3	AAY44596	EscFv#125
34	484.5	78.5	116	2	AAW95481	Mouse der
35	483	78.3	112	5	AAE15811	Human mAb
36	479.5	77.7	467	6	AAE38408	Mouse vir
37	478.5	77.6	118	2	AAY52760	Anti-tiss
38	474.5	76.9	214	6	ABP96759	TSH recep
39	474.5	76.9	214	6	ABP96760	TSH recep
40	473.5	76.7	116	2	AAW39889	Heavy cha
41	472	76.5	118	4	AAE12045	Murine an
42	472	76.5	118	7	AAE39613	Murine 5G
43	471.5	76.4	116	2	AAW71882	Anti-Fas
44	471.5	76.4	116	3	AAB12919	Anti-huma
45	471.5	76.4	130	2	AAW71886	Anti-Fas

ALIGNMENTS

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RESULT 1
AAW71288
ID   AAW71288 standard; protein; 117 AA.
XX
AC   AAW71288;
XX
DT   10-DEC-1998  (first entry)
XX
DE   Human anti-tissue factor heavy chain variable region.
XX
KW   Human; anti-tissue factor light chain variable region; H36.D2.B7;
KW   anti-tissue factor heavy chain variable region; inhibition; antibody;
KW   blood coagulation; thrombosis; restenosis; thromboembolic condition;
KW   cardiovascular; infection; neoplastic disease; clot; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO9840408-A1.
XX
PD   17-SEP-1998.
XX
PF   10-MAR-1998;       98WO-US004644.
XX
PR   10-MAR-1997;       97US-0814806.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Wong HC, Jiao J, Nieves EL, Luepschen L;
XX
DR   WPI; 1998-520804/44.
DR   N-PSDB; AAV54962.
XX
PT   New antibody to human tissue factor - used for, e.g. treating thrombosis
PT   or restenosis or thromboembolic conditions associated with
PT   cardiovascular, infectious or neoplastic disease.
XX
PS   Claim 12; Fig 1B; 53pp; English.
XX
CC   The present sequence represents the human anti-tissue factor heavy chain
CC   variable region from an antibody that binds native human tissue factor
CC   (TF) and does not bind non-native TF. The antibody capable of
CC   specifically-binding native TF may be used for inhibiting blood
CC   coagulation and also for reducing TF levels in a mammal. The antibodies
CC   can be used, e.g. to treat thromboses-particularly to prevent or inhibit
CC   restenosis, or other thromboses following an invasive medical procedure
CC   such as arterial or cardiac surgery (e.g. angioplasty, endarterectomy,
CC   deployment of a stent, use of catheter, graft implantation or use of an
```

CC   arteriovenous shunt). The antibodies can also be used as a carrier for
CC   drugs, particularly pharmaceuticals targeted for interaction with a blood
CC   clot such as streptokinase, tissue plasminogen activator (t-PA) or
CC   urokinase, or a cytotoxic agent by conjugating a suitable toxin to the
CC   antibody. Further the antibodies can be used for treating a
CC   thromboembolic condition associated with cardiovascular disease, an
CC   infectious disease, a neoplastic disease or as a thrombolytic agent. The
CC   antibodies can also be used for detection and diagnosis
XX
SQ   Sequence 117 AA;

Query Match   100.0%;   Score 617; DB 2; Length 117;
Best Local Similarity 99.1%;   Pred. No. 4e-49;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   1 EIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 2
ABR42700
ID   ABR42700 standard; protein; 117 AA.
XX
AC   ABR42700;
XX
DT   26-AUG-2003 (first entry)
XX
DE   Anti-tissue factor antibody H36.D2.B7 VH region.
XX
KW   Tissue factor; antibody; H36.D2.B7; anticoagulant; cytostatic;
KW   antiinflammatory; mouse.
XX
OS   Mus sp.
XX
FH   Key   Location/Qualifiers
FT   Region   30..35
FT   /note="complementarity determining region 1"
FT   Region   50..66
FT   /note="complementarity determining region 2"
FT   Misc-difference 86
FT   /note="apparently encoded by TATT"
FT   Region   99..106
FT   /note="complementarity determining region 3"
XX
PN   WO200037911-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-00990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
DR   N-PSDB; ACC58569.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
PS   Example 1; Fig 1B; 110pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain variable

CC   region (VH) of anti-recombinant human tissue factor (TF) murine antibody
CC   H36.D2.B7 (ATCC HB-12255). The invention relates to antibodies,
CC   especially humanized H36.D2.B7, that provide superior anticoagulant
CC   activity by binding native human TF with high affinity and specificity.
CC   The antibodies bind human TF, either alone or present in a TF:Factor VIIa
CC   complex, effectively preventing Factor X (or Factor IX) binding to TF or
CC   the complex, and thereby reducing blood coagulation. The humanized
CC   antibodies are useful for inhibiting blood coagulation or blood clot
CC   formation, angiogenesis, tumour metastases or inflammation in a mammal.
CC   They are also useful as drug carriers, as cytotoxic agents, for reducing
CC   TF levels in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match   100.0%;   Score 617; DB 6; Length 117;
Best Local Similarity 99.1%;   Pred. No. 4e-49;
Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
         ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   1 EIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 3
ABR42718
ID   ABR42718 standard; protein; 117 AA.
XX
AC   ABR42718;
XX
DT   26-AUG-2003 (first entry)
XX
DE   Anti-tissue factor chimeric antibody cH36 VH region.
XX
KW   Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW   antiinflammatory; mouse.
XX
OS   Mus sp.
XX
FH   Key   Location/Qualifiers
FT   Region   1..30
FT   /note="framework 1"
FT   Region   31..35
FT   /note="complementarity determining region 1"
FT   Region   36..49
FT   /note="framework 2"
FT   Region   50..66
FT   /note="complementarity determining region 2"
FT   Region   67..98
FT   /note="framework 3"
FT   Region   99..106
FT   /note="complementarity determining region 3"
FT   Region   107..117
FT   /note="framework 4"
XX
PN   WO200037911-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-00990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
XX

```
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
PS   Claim 12; Fig 13; 110pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain variable
CC   region (VH) of anti-recombinant human tissue factor (TF) mouse-human
CC   chimeric antibody CH36. This sequence has been humanized in a series of
CC   steps (see ABR42719-34) to provide a humanized VH sequence for use in the
CC   production of an anti-human TF humanized antibody. Humanized antibodies
CC   of the invention provide superior anticoagulant activity by binding
CC   native human TF with high affinity and specificity. The antibodies bind
CC   human TF, either alone or present in a TF:Factor VIIa complex,
CC   effectively preventing Factor X (or Factor IX) binding to TF or the
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match             100.0%;  Score 617;  DB 6;  Length 117;
Best Local Similarity   99.1%;   Pred. No. 4e-49;
Matches 116;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 4
ADL35005
ID   ADL35005 standard; protein; 117 AA.
XX
AC   ADL35005;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Murine anti-tissue factor heavy chain antibody protein SeqID 4.
XX
KW   murine; mouse; humanised antibody; variable domain; framework region; FR;
KW   huFR; immune system molecule; H36.D2.B7; anti-tissue factor.
XX
OS   Mus sp.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 25
FT                  /note= "Encoded by TCT"
XX
PN   WO200420579-A2.
XX
PD   11-MAR-2004.
XX
PF   06-AUG-2003; 2003WO-US024637.
XX
PR   29-AUG-2002; 2002US-00230880.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Wong HC, Stinson JR, Mosquera LA;
XX
DR   WPI; 2004-239169/22.
DR   N-PSDB; ADL35004.
XX
PT   Producing humanized antibodies for diagnostic and therapeutic purposes
PT   comprises optimizing similarity between individual antibody framework
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PT   regions to help identify human framework regions suitable for making the
PT   antibodies.
XX
PS   Disclosure; SEQ ID NO 4; 137pp; English.
XX
CC   This invention relates to a novel method for producing a humanised
CC   antibody variable (V) domain or its fragment by optimising sequence
CC   similarity between individual antibody framework regions (FRs) in order
CC   to identify suitable human FRs (huFRs). Specifically, it refers to novel
CC   immune system molecules i.e. humanised monoclonal antibodies that exhibit
CC   suitable binding affinity with reduced immunogenicity in humans. The
CC   present invention describes a method of mutagenising DNA of non-human FRs
CC   to encode humanised FRs having an amino acid sequence that is
CC   substantially identical to the selected human FR previously identified
CC   through sequence similarity searching. As such, this method provides
CC   humanised light or heavy chain v domains of the sequence huFR1-CDR1-huFR2
CC   -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic
CC   products to treat and/or diagnose diseases in humans and animals.
CC   Furthermore, the method expands the number of best fit possibilities that
CC   can be generated and provides a rational basis for assembling nearly all
CC   humanised immune system molecules of interest. This polypeptide sequence
CC   is a murine anti-tissue factor heavy chain antibody H36.D2.B7 protein of
CC   the invention.
XX
SQ   Sequence 117 AA;

Query Match             99.8%;   Score 616;  DB 8;  Length 117;
Best Local Similarity   100.0%;  Pred. No. 5e-49;
Matches 117;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 5
ADU06810
ID   ADU06810 standard; protein; 117 AA.
XX
AC   ADU06810;
XX
DT   10-FEB-2005  (first entry)
XX
DE   Murine H36.D2.B7 antibody VH SEQ ID NO:4.
XX
KW   septic shock syndrome; tissue factor; antibacterial; immunosuppressive;
KW   antibody; antibody therapy.
XX
OS   Mus musculus.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 25
FT                  /note= "Encoded by TCT"
FT                  /note= "Variable amino acid"
FT   Region         30..35
FT                  /label= CDR1
FT   Region         50..66
FT                  /label= CDR2
FT   Region         99..106
FT                  /label= CDR3
XX
PN   US2004229282-A1.
XX
PD   18-NOV-2004.
XX
PF   22-JAN-2004; 2004US-00764140.
XX
PR   10-MAR-1997; 97US-00814806.
PR   16-APR-1999; 99US-00293854.
```

PR   12-NOV-2002; 2002US-00293417.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Wong HC, Jiao J;
XX
DR   WPI; 2004-813246/80.
DR   N-PSDB; ADU06809.
XX
PT   Treating or preventing septic shock syndrome in mammal, involves
PT   administering antibody that binds native human tissue factor and does not
PT   substantially bind non-native tissue factor.
XX
PS   Claim 44; SEQ ID NO 4; 28pp; English.
XX
CC   The invention relates to a novel method for treating or preventing (M1)
CC   septic shock syndrome in a mammal, involving administering to the mammal
CC   an effective amount of an antibody that binds native human tissue factor
CC   and does not substantially bind non-native tissue factor, where the
CC   factor X binding to the complex is inhibited and the administration is
CC   sufficient to prevent or treat the septic shock syndrome in the mammal.
CC   In (M1), the antibody has the binding specificity for native human tissue
CC   factor about to or greater than H36.D2.B7 (ATCC HB-12255), and is a
CC   monoclonal chimeric antibody. An antibody of the invention has
CC   antibacterial and immunosuppressive activity, and acts as an inhibitor of
CC   binding between factor X or factor VIa and tissue factor/factor VIIa
CC   complex. The present sequence represents the heavy chain variable region
CC   of the murine antibody of the invention, H36.D2.B7.
XX
SQ   Sequence 117 AA;

Query Match   99.8%; Score 616; DB 8; Length 117;
Best Local Similarity   100.0%; Pred. No. 5e-49;
Matches   117; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 6
ADW07328
ID   ADW07328 standard; protein; 117 AA.
XX
AC   ADW07328;
XX
DT   07-APR-2005 (first entry)
XX
DE   Mouse anti-tissue factor antibody H36.D2.B7 VH.
XX
KW   Blood-clotting; heavy chain variable region; inflammation;
KW   antiinflammatory; antibody; tissue factor; sepsis;
KW   disseminated intravascular coagulation; anticoagulant;
KW   hematological disease; thrombosis; lung injury; respiratory-gen.;
KW   respiratory distress syndrome; immunosuppressive; Antibacterial;
KW   Antiarthritic; Antianemic; anemia; rheumatoid arthritis;
KW   glomerulonephritis; multiple sclerosis; psoriasis; sjogren's syndrome;
KW   inflammatory bowel disease.
XX
OS   Mus sp.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference 25
FT   /label= UNKNOWN
FT   /note= "Encoded by TCT"
XX
PN   WO2005004793-A2.
XX
PD   20-JAN-2005.

XX
PF   04-JUN-2004; 2004WO-US017900.
PR
PR   19-JUN-2003; 2003US-0480254P.
PR   22-JAN-2004; 2004US-0538892P.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Egan JO;
XX
DR   WPI; 2005-091964/10.
DR   N-PSDB; ADW07327.
XX
PT   Preventing or treating sepsis or inflammation in mammals comprises
PT   administering a humanized or chimeric antibody that binds to a human
PT   tissue factor to form a complex in which factor X or IX binding to the
PT   complex is inhibited.
XX
PS   Disclosure; SEQ ID NO 4; 109pp; English.
XX
CC   The invention relates to preventing or treating a sepsis or inflammatory
CC   disease in a mammal comprising administering to the mammal a therapeutic
CC   amount of at least one humanized antibody, chimeric antibody, or their
CC   fragment that binds specifically to tissue factor (TF) to form a complex,
CC   where factor X or IX binding to the complex is inhibited and the
CC   administration prevents or treats the sepsis in the mammal. Also included
CC   are a kit for performing the above method and reducing an inflammatory
CC   cytokine production in a mammal. The inflammatory disease is associated
CC   with arthritis (preferably rheumatoid arthritis), glomerulonephritis,
CC   multiple sclerosis, psoriasis, Sjogren's syndrome, or inflammatory bowel
CC   disease. The method also treats or prevents a sepsis-induced anemia or a
CC   sepsis-related condition in a mammal, where the sepsis-related condition
CC   is DIC, fibrin deposition, thrombosis, lung injury, or sepsis-associated
CC   renal disorder. The lung injury is acute lung injury (ALI) or acute
CC   respiratory distress syndrome (ARDS). The sepsis-associated renal
CC   disorder is acute tubular necrosis. The methods and kit are useful for
CC   preventing or treating sepsis or sepsis-related conditions (e.g. DIC or
CC   anemia) or inflammatory diseases (e.g. arthritis). The humanized
CC   antibodies are based on the chimeric antibody cH36 which comprises the
CC   light and heavy chain variable regions (VL or VH) of an anti-TF antibody
CC   fused to the human IgG4 heavy and kappa light constant regions. The CDRs
CC   (complementarity determining region) and FRs (framework regions) are then
CC   humanized. The present sequence represents the light or heavy chain
CC   variable region of the anti-TF antibody (wild-type).
XX
SQ   Sequence 117 AA;

Query Match   99.8%; Score 616; DB 9; Length 117;
Best Local Similarity   100.0%; Pred. No. 5e-49;
Matches   117; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 7
AD240939
ID   AD240939 standard; protein; 117 AA.
XX
AC   AD240939;
XX
DT   14-JUL-2005 (first entry)
XX
DE   H36.D2.B7 anti-tissue factor heavy chain variable region.
XX
KW   antibody; tissue factor; blood-clotting; anticoagulant; vasotropic;
KW   thrombolytic; cardiovascular disease; infectious disease; neoplasm;
KW   thrombosis; restenosis; heavy chain variable region.

```
XX    OS    Homo sapiens.
OS          Synthetic.
XX
FH    Key          Location/Qualifiers
FT    Misc-difference  25
FT                 /label= unkown
FT                 /note= "encoded by TCT"
XX
PN    US2005089929-A1.
XX
PD    28-APR-2005.
XX
PF    11-JUL-2003; 2003US-0061B338.
XX
PR    10-MAR-1997;  97US-00814806.
PR    16-APR-1999;  99US-00293854.
PR    12-NOV-2002; 2002US-00293417.
XX
PA    (SUNO-) SUNOL MOLECULAR CORP.
XX
PI    Jiao J, Wong HC, Wen J;
XX
DR    WPI; 2005-344279/35.
DR    N-PSDB; AD240938.
XX
PT    Antibodies binding to native human tissue factor without substantial
PT    binding to non-native tissue factor, useful for inhibiting blood
PT    coagulation, for reducing tissue factor levels in a mammal, and for
PT    detecting tissue factor.
XX
PS    Claim 12; SEQ ID NO 4; 36pp; English.
XX
CC    The invention relates to an antibody (I) that binds native human tissue
CC    factor and does not substantially bind non-native tissue factor. Also
CC    described: (1) an isolated nucleic acid (II) comprising a sequence
CC    encoding at least a portion of an antibody that binds native human tissue
CC    factor; (2) a recombinant vector (IV) comprising (II), where (IV) can
CC    express at least a portion of an antibody that binds native human tissue
CC    factor; (3) a host cell (V) comprising (IV); (4) inhibiting (M1) blood
CC    coagulation in a mammal by administering the antibody, where the antibody
CC    complexes with native tissue factor and factor X binding to the complex
CC    is inhibited; (5) reducing (M2) tissue factor levels in a mammal by
CC    administering the antibody covalently linked to a cell toxin or to an
CC    effector molecule to provide complement-fixing ability and antibody-
CC    dependent cell-mediated cytotoxicity, where the antibody contacts cells
CC    expressing tissue factor to reduce tissue factor levels in the mammal;
CC    and (6) detecting (M3) tissue factor in a biological sample comprising
CC    contacting the sample with the antibody (I), where the antibody is
CC    monoclonal. (I) is useful for inhibiting blood coagulation in a mammal
CC    (preferably human), for reducing tissue factor levels in a mammal, and
CC    for detecting tissue factor in a biological sample. (I) can be used in
CC    the treatment of a thromboembolic condition associated with
CC    cardiovascular disease, an infectious disease, or a neoplastic disease,
CC    such as thrombosis and restenosis. The antibodies of the invention
CC    (especially H36.D2.B7 (secreted by hybridoma ATCC HB-12255)) bind
CC    strongly to a conformational epitope in native human tissue factor and do
CC    not substantially bind to non-native or denatured tissue factor. The
CC    antibodies prevent conversion of factor X to its activated form factor
CC    Xa. The present sequence represents the H36.D2.B7 anti-tissue factor
CC    heavy chain variable region.
XX
SQ    Sequence 117 AA;

Query Match             99.8%;  Score 616;  DB 9;  Length 117;
Best Local Similarity   100.0%;  Pred. No. 5e-49;
Matches  117;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy    61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
```

```
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match             99.0%;  Score 611; DB 6; Length 117;
Best Local Similarity   97.4%;  Pred. No. 1.4e-48;
Matches 114; Conservative  2; Mismatches  1; Indels  0; Gaps  0;

Qy    1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          ||||||||||||||||||||||| || |||||||||||||||| ||||||||||||||||
Db    1 QIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSPGKGLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTVTVSS 117


RESULT 9
ABR42720
ID   ABR42720 standard; protein; 117 AA.
XX
AC   ABR42720;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-tissue factor humanized antibody VH region HC-02.
XX
KW   Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW   antiinflammatory; human; mouse.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key              Location/Qualifiers
FT   Region           1..30
FT                    /note= "framework 1"
FT   Misc-difference  1
FT                    /note= "wild-type Glu substituted by Gln"
FT   Region           31..35
FT                    /note= "complementarity determining region 1"
FT   Region           36..49
FT                    /note= "framework 2"
FT   Misc-difference  41
FT                    /note= "wild-type His substituted by Pro"
FT   Misc-difference  44
FT                    /note= "wild-type Ser substituted by Gly"
FT   Region           50..66
FT                    /note= "complementarity determining region 2"
FT   Region           67..98
FT                    /note= "framework 3"
FT   Region           99..106
FT                    /note= "complementarity determining region 3"
FT   Region           107..117
FT                    /note= "framework 4"
FT   Misc-difference  113
FT                    /note= "wild-type Leu substituted by Val"
XX
PN   WO200303791l-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-00990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
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```
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
PS   Claim 12; Fig 13; 110pp; English.
XX
CC   The present sequence is the protein sequence of a humanized version, HC-
CC   02, of the heavy chain variable region (VH) of anti-recombinant human
CC   tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR
CC   mutagenesis steps was used to introduce mutations into the cH36 sequence
CC   to fully humanize the VH region (see ABR42719-31) and hence for the
CC   production of an anti-human TF humanized antibody. Humanized antibodies
CC   of the invention provide superior anticoagulant activity by binding
CC   native human TF with high affinity and specificity. The antibodies bind
CC   human TF, either alone or present in a TF:Factor VIIa complex,
CC   effectively preventing Factor X (or Factor IX) binding to TF or the
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match             96.8%;  Score 597; DB 6; Length 117;
Best Local Similarity   95.7%;  Pred. No. 2.8e-47;
Matches 112; Conservative  2; Mismatches  3; Indels  0; Gaps  0;

Qy    1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          ||||||||||||||||||||||| || |||||||||||||||| ||||||||||||||||
Db    1 QIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSPGKGLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
          ||||||||||||||||||||||||||||||||||||||||||||||:|||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTVTVSS 117


RESULT 10
ABR42721
ID   ABR42721 standard; protein; 117 AA.
XX
AC   ABR42721;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-tissue factor humanized antibody VH region HC-03.
XX
KW   Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW   antiinflammatory; mouse; human.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key              Location/Qualifiers
FT   Region           1..30
FT                    /note= "framework 1"
FT   Misc-difference  1
FT                    /note= "wild-type Glu substituted by Gln"
FT   Region           31..35
FT                    /note= "complementarity determining region 1"
FT   Region           36..49
FT                    /note= "framework 2"
FT   Misc-difference  41
FT                    /note= "wild-type His substituted by Pro"
FT   Misc-difference  44
FT                    /note= "wild-type Ser substituted by Gly"
FT   Region           50..66
```

```
FT   Region
FT                   /note= "complementarity determining region 2"
FT   Region          67..98
FT                   /note= "framework 3"
FT   Misc-difference 87
FT                   /note= "wild-type Thr substituted by Arg"
FT   Misc-difference 89
FT                   /note= "wild-type Asp substituted by Glu"
FT   Misc-difference 91
FT                   /note= "wild-type Ser substituted by Thr"
FT   Region          99..106
FT                   /note= "complementarity determining region 3"
FT   Region          107..117
FT                   /note= "framework 4"
FT   Misc-difference 113
FT                   /note= "wild-type Leu substituted by Val"
XX
PN   WO2003037911-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-00990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
CC   Claim 12; Fig 13; 110pp; English.
XX
CC   The present sequence is the protein sequence of a humanized version, HC-
CC   03, of the heavy chain variable region (VH) of anti-recombinant human
CC   tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR
CC   mutagenesis steps was used to introduce mutations into the cH36 sequence
CC   to fully humanize the VH region (see ABR42719-31) and hence for the
CC   production of an anti-human TF humanized antibody. Humanized antibodies
CC   of the invention provide superior anticoagulant activity by binding
CC   native human TF with high affinity and specificity. The antibodies bind
CC   human TF, either alone or present in a TF:Factor VIIa complex,
CC   effectively preventing Factor X (or Factor IX) binding to TF or the
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match             94.7%;  Score 584;  DB 6;  Length 117;
Best Local Similarity   93.2%;  Pred. No. 4.4e-46;
Matches  109;  Conservative  4;  Mismatches  4;  Indels  0;  Gaps  0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              | |||||||||||||||||||||| ||||||||||||||| |: ||||||||||||||||
Db          1 QIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSPGKGLEWIGYIDPYNGITIY 60

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              |||||||||||||||||||||||| :|: |||||||||||||||||||||||||||
Db         61 DQNFKGKATLTVDKSSTAFMHLNSLRSEDTAVVFCARDVTTALDFWGQGTTVTVSS 117

RESULT 11
ABR42722
ID   ABR42722  standard; protein;  117 AA.
XX
AC   ABR42722;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-tissue factor humanized antibody VH region HC-04.
XX
KW   Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW   antiinflammatory; mouse; human.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FH
FT   Region          1..30
FT                   /note= "framework 1"
FT   Misc-difference 1
FT                   /note= "wild-type Glu substituted by Gln"
FT   Region          31..35
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FT   Region          36..49
FT                   /note= "framework 2"
FT   Misc-difference 41
FT                   /note= "wild-type His substituted by Pro"
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FT                   /note= "wild-type Ser substituted by Gly"
FT   Region          50..66
FT                   /note= "complementarity determining region 2"
FT   Region          67..98
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FT   Misc-difference 82
FT                   /note= "wild-type His substituted by Glu"
FT   Misc-difference 84
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FT                   /note= "wild-type Thr substituted by Arg"
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FT                   /note= "wild-type Asp substituted by Glu"
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FT   Region          99..106
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FT   Region          107..117
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FT   Misc-difference 113
FT                   /note= "wild-type Leu substituted by Val"
XX
PN   WO2003037911-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-00990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
CC   Claim 12; Fig 13; 110pp; English.
XX
CC   The present sequence is the protein sequence of a humanized version, HC-
CC   04, of the heavy chain variable region (VH) of anti-recombinant human
CC   tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR
CC   mutagenesis steps was used to introduce mutations into the cH36 sequence
```

```
CC   to fully humanize the VH region (see ABR42719-31) and hence for the
CC   production of an anti-human TF humanized antibody. Humanized antibodies
CC   of the invention provide superior anticoagulant activity by binding
CC   native human TF with high affinity and specificity. The antibodies bind
CC   human TF, either alone or present in a TF:Factor VIIa complex,
CC   effectively preventing Factor X (or Factor IX) binding to TF or the
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match             92.5%;  Score 571;  DB 6;  Length 117;
Best Local Similarity   91.5%;  Pred. No. 7e-45;
Matches  107;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNYVWVRQSHGKSLEWIGYIDPYNGITIY 60
             :||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||||
Db         1 QIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSPGKGLEWIGYIDPYNGITIY 60

Qy        61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
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Db        61 DQNFKGKATLTVDKSSTAFMELSSLRSEDTAVYFCARDVTTALDFWGQGTTVTVSS 117

RESULT 12
ABR42723
ID   ABR42723 standard; protein; 117 AA.
XX
AC   ABR42723;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-tissue factor humanized antibody VH region HC-05.
XX
KW   Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW   antiinflammatory; mouse; human.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /note= "framework 1"
FT   Misc-difference 1
FT                   /note= "wild-type Glu substituted by Gln"
FT   Region          31..35
FT                   /note= "complementarity determining region 1"
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FT                   /note= "framework 2"
FT   Misc-difference 41
FT                   /note= "wild-type His substituted by Pro"
FT   Misc-difference 44
FT                   /note= "wild-type Ser substituted by Gly"
FT   Region          50..66
FT                   /note= "complementarity determining region 2"
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FT                   /note= "framework 3"
FT   Misc-difference 76
FT                   /note= "wild-type Ser substituted by Thr"
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FT   Misc-difference 80
FT                   /note= "wild-type Phe substituted by Tyr"
FT   Misc-difference 82
FT                   /note= "wild-type His substituted by Glu"
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FT                   /note= "wild-type Asn substituted by Ser"
FT   Misc-difference 87
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FT                   /note= "wild-type Asp substituted by Glu"
FT   Misc-difference 91
FT                   /note= "wild-type Ser substituted by Thr"
FT   Region          99..106
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FT                   /note= "framework 4"
FT   Misc-difference 113
FT                   /note= "wild-type Leu substituted by Val"
XX
PN   WO200303791l-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-00990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J,  Wong HC,  Nieves EL,  Mosquera LA;
XX
DR   WPI; 2003-468399/44.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
PS   Claim 12; Fig 13; 110pp; English.
XX
CC   The present sequence is the protein sequence of a humanized version, HC-
CC   05, of the heavy chain variable region (VH) of anti-recombinant human
CC   tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR
CC   mutagenesis steps was used to introduce mutations into the cH36 sequence
CC   to fully humanize the VH region (see ABR42719-31) and hence for the
CC   production of an anti-human TF humanized antibody. Humanized antibodies
CC   of the invention provide superior anticoagulant activity by binding
CC   native human TF with high affinity and specificity. The antibodies bind
CC   human TF, either alone or present in a TF:Factor VIIa complex,
CC   effectively preventing Factor X (or Factor IX) binding to TF or the
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match             90.9%;  Score 561;  DB 6;  Length 117;
Best Local Similarity   88.9%;  Pred. No. 5.8e-44;
Matches  104;  Conservative    8;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNYVWVRQSHGKSLEWIGYIDPYNGITIY 60
             :||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||||
Db         1 QIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSPGKGLEWIGYIDPYNGITIY 60

Qy        61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
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Db        61 DQNFKGKATLTVDKSSTAYMELSSLRSEDTAVYFCARDVTTALDFWGQGTTVTVSS 117

RESULT 13
ABR42730
ID   ABR42730 standard; protein; 117 AA.
XX
AC   ABR42730;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-tissue factor humanized antibody VH region HC-09.
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XX
KW   Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW   antiinflammatory; mouse; human.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /note= "framework 1"
FT   Misc-difference 1
FT                   /note= "wild-type Glu substituted by Gln"
FT   Misc-difference 5
FT                   /note= "wild-type Val substituted by Gln"
FT   Misc-difference 19
FT                   /note= "wild-type Gln substituted by Arg"
FT   Misc-difference 24
FT                   /note= "wild-type Thr substituted by Ala"
FT   Region          31..35
FT                   /note= "complementarity determining region 1"
FT   Region          36..49
FT                   /note= "framework 2"
FT   Misc-difference 41
FT                   /note= "wild-type His substituted by Pro"
FT   Misc-difference 44
FT                   /note= "wild-type Ser substituted by Gly"
FT   Region          50..66
FT                   /note= "complementarity determining region 2"
FT   Region          67..98
FT                   /note= "framework 3"
FT   Misc-difference 76
FT                   /note= "wild-type Ser substituted by Thr"
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FT   Misc-difference 82
FT                   /note= "wild-type His substituted by Glu"
FT   Misc-difference 84
FT                   /note= "wild-type Asn substituted by Ser"
FT   Misc-difference 87
FT                   /note= "wild-type Thr substituted by Arg"
FT   Misc-difference 89
FT                   /note= "wild-type Asp substituted by Glu"
FT   Misc-difference 91
FT                   /note= "wild-type Ser substituted by Thr"
FT   Region          99..106
FT                   /note= "complementarity determining region 3"
FT   Region          107..117
FT                   /note= "framework 4"
FT   Misc-difference 113
FT                   /note= "wild-type Leu substituted by Val"
XX
PN   WO200303791-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-00990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
```

```
XX
PS   Claim 12; Fig 13; 110pp; English.
XX
CC   The present sequence is the protein sequence of a humanized version, HC-
CC   09, of the heavy chain variable region (VH) of anti-recombinant human
CC   tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR
CC   mutagenesis steps was used to introduce mutations into the cH36 sequence
CC   to fully humanize the VH region (see ABR42719-31) and hence for the
CC   production of an anti-human TF humanized antibody. Humanized antibodies
CC   of the invention provide superior anticoagulant activity by binding
CC   native human TF with high affinity and specificity. The antibodies bind
CC   human TF, either alone or present in a TF:Factor VIIa complex,
CC   effectively preventing Factor X (or Factor IX) binding to TF or the
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

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              :||||||||||||||||| :||||| :||||||||||||||| |:||||||||||||||
Db          1 QIQLVQSGPELVKPGASVRVSCKASGYSFTDYNVYWRQSPGKGLEWIGYIDPYNGITIY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              ||||||||||||||||||:| |::||| :|:||||||||||||||||||||:|||||
Db         61 DQNFKGKATLTVDKSSTTAYMELSSLRSEDTAVYFCARDVTTALDFWGQGTTVTVSS 117

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ID   ABR42731 standard; protein; 117 AA.
XX
AC   ABR42731;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-tissue factor humanized antibody VH region HC-10.
XX
KW   Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW   antiinflammatory; mouse; human.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /note= "framework 1"
FT   Misc-difference 1
FT                   /note= "wild-type Glu substituted by Gln"
FT   Misc-difference 5
FT                   /note= "wild-type Val substituted by Gln"
FT   Misc-difference 19
FT                   /note= "wild-type Gln substituted by Arg"
FT   Misc-difference 24
FT                   /note= "wild-type Thr substituted by Ala"
FT   Region          31..35
FT                   /note= "complementarity determining region 1"
FT   Region          36..49
FT                   /note= "framework 2"
FT   Misc-difference 41
FT                   /note= "wild-type His substituted by Pro"
FT   Misc-difference 44
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FT   Region          50..66
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Qy   61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
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RESULT 15
ABR42724
ID   ABR42724 standard; protein; 117 AA.
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AC   ABR42724;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-tissue factor humanized antibody VH region HC-06.
XX
KW   Tissue factor; humanization; antibody; anticoagulant; cytostatic;
KW   antinflammatory; mouse; human.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
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FH   Key             Location/Qualifiers
FT   Region          1..30
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FT   Region          36..49
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FT                   /note= "wild-type His substituted by Pro"
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FT                   /note= "wild-type Ser substituted by Gly"
FT   Region          50..66
FT                   /note= "complementarity determining region 2"
FT   Region          67..98
FT                   /note= "framework 3"
FT   Misc-difference 76
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FT                   /note= "wild-type Thr substituted by Ser"
FT   Misc-difference 80
FT                   /note= "wild-type Phe substituted by Tyr"
FT   Misc-difference 82
FT                   /note= "wild-type His substituted by Glu"
FT   Misc-difference 84
FT                   /note= "wild-type Asn substituted by Ser"
FT   Misc-difference 87
FT                   /note= "wild-type Thr substituted by Arg"
FT   Misc-difference 89
FT                   /note= "wild-type Asp substituted by Glu"
FT   Misc-difference 91
FT                   /note= "wild-type Ser substituted by Thr"
FT   Region          99..106
FT                   /note= "complementarity determining region 3"
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FT                   /note= "framework 4"
FT   Misc-difference 113
FT                   /note= "wild-type Leu substituted by Val"
FT   Misc-difference 115
FT                   /note= "wild-type Leu substituted by Val"
XX
PN   WO200303791l-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-0090586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
PS   Claim 12; Fig 13; 110pp; English.
XX
CC   The present sequence is the protein sequence of a humanized version, HC-
CC   10, of the heavy chain variable region (VH) of anti-recombinant human
CC   tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR
CC   mutagenesis steps was used to introduce mutations into the cH36 sequence
CC   to fully humanize the VH region (see ABR42719-31) and hence for the
CC   production of an anti-human TF humanized antibody. Humanized antibodies
CC   of the invention provide superior anticoagulant activity by binding
CC   native human TF with high affinity and specificity. The antibodies bind
CC   human TF, either alone or present in a TF:Factor VIIa complex,
CC   effectively preventing Factor X (or Factor IX) binding to TF or the
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match             87.8%;  Score 542;  DB 6;  Length 117;
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PR   21-NOV-2001; 2001US-0990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
PS   Claim 12; Fig 13; 110pp; English.
XX
CC   The present sequence is the protein sequence of a humanized version, HC-
CC   06, of the heavy chain variable region (VH) of anti-recombinant human
CC   tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR
CC   mutagenesis steps was used to introduce mutations into the cH36 sequence
CC   to fully humanize the VH region (see ABR42719-31) and hence for the
CC   production of an anti-human TF humanized antibody. Humanized antibodies
CC   of the invention provide superior anticoagulant activity by binding
CC   native human TF with high affinity and specificity. The antibodies bind
CC   human TF, either alone or present in a TF:Factor VIIa complex,
CC   effectively preventing Factor X (or Factor IX) binding to TF or the
CC   complex, and thereby reducing blood coagulation. The humanized antibodies
CC   are useful for inhibiting blood coagulation or blood clot formation,
CC   angiogenesis, tumour metastases or inflammation in a mammal. They are
CC   also useful as drug carriers, as cytotoxic agents, for reducing TF levels
CC   in mammals, and for in vivo diagnosis
XX
SQ   Sequence 117 AA;

Query Match   87.5%; Score 540; DB 6; Length 117;
Best Local Similarity   85.5%; Pred. No. 5e-42;
Matches 100; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
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Db   1 QMQLQQSGGGELVKPGASVRVSCKASGYSFTDYNVTWVRQSPGKGLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
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Db   61 DQNFKGKATLTVDKSTSTAYMELSSLRSEDTAVYFCARDVTTALDFWGQGTTVTVSS 117

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OM protein - protein search, using sw model

Run on: April 18, 2006, 13:39:50 ; Search time 47 Seconds
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Post-processing: Minimum Match 0%
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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2	616	99.8	117	2	US-09-293-854-4	Sequence 4, Appli
3	521.5	84.5	118	2	US-09-647-468-139	Sequence 139, App
4	521.5	84.5	118	2	US-09-647-468-140	Sequence 140, App
5	521.5	84.5	137	2	US-09-647-468-153	Sequence 153, App
6	521.5	84.5	137	2	US-09-647-468-154	Sequence 154, App
7	484.5	78.5	116	1	US-08-273-146-55	Sequence 55, Appl
8	478.5	77.6	118	2	US-09-647-468-144	Sequence 144, App
9	478.5	77.6	137	2	US-09-647-468-158	Sequence 158, App
10	473.5	76.7	116	1	US-08-672-345C-105	Sequence 105, App
11	473.5	76.7	116	1	US-09-214-095D-90	Sequence 90, Appl
12	473.5	76.7	116	2	US-09-940-727B-90	Sequence 90, Appl
13	472	76.5	118	2	US-09-802-083-5	Sequence 5, Appli
14	469.5	76.1	118	2	US-09-647-468-143	Sequence 143, App
15	469.5	76.1	137	2	US-09-647-468-157	Sequence 157, App
16	469	76.0	301	2	US-08-656-906-25	Sequence 25, Appl
17	469	76.0	301	1	US-09-217-847-25	Sequence 25, Appl
18	468.5	75.9	116	1	US-08-672-345C-106	Sequence 106, App
19	467.5	75.8	116	1	US-07-634-278-56	Sequence 56, Appl
20	467.5	75.8	116	1	US-08-477-728-56	Sequence 56, Appl
21	467.5	75.8	116	1	US-08-474-040-56	Sequence 56, Appl
22	467.5	75.8	116	1	US-08-487-200-56	Sequence 56, Appl
23	467.5	75.8	116	2	US-08-484-537-56	Sequence 56, Appl
24	467.5	75.8	135	1	US-07-634-278-69	Sequence 69, Appl
25	467.5	75.8	135	1	US-08-477-728-69	Sequence 69, Appl
26	467.5	75.8	135	1	US-08-474-040-69	Sequence 69, Appl
27	467.5	75.8	135	1	US-08-487-200-69	Sequence 69, Appl
28	467.5	75.8	135	1	US-08-137-117D-27	Sequence 27, Appl
29	467.5	75.8	135	1	US-08-436-717-27	Sequence 27, Appl
30	467.5	75.8	135	2	US-08-484-537-69	Sequence 69, Appl
31	465.5	75.4	116	1	US-08-672-345C-14	Sequence 14, Appl
32	465.5	75.4	116	2	US-09-214-095D-14	Sequence 14, Appl
33	465.5	75.4	116	2	US-09-940-727B-14	Sequence 14, Appl
34	462	74.9	132	2	US-08-434-000A-14	Sequence 14, Appl
35	462	74.9	132	2	US-09-312-157-14	Sequence 14, Appl
36	462	74.9	132	2	US-09-717-888-14	Sequence 14, Appl
37	454	73.6	130	2	US-09-556-605-3	Sequence 3, Appli
38	453.5	73.5	143	2	US-09-301-593-26	Sequence 26, Appl
39	453.5	73.5	472	2	US-09-301-593-30	Sequence 30, Appl
40	451	73.1	264	2	US-10-114-716A-46	Sequence 46, Appl
41	450	72.9	115	1	US-08-672-345C-16	Sequence 16, Appl
42	450	72.9	115	2	US-09-214-095D-16	Sequence 16, Appl
43	450	72.9	115	2	US-09-940-727B-16	Sequence 16, Appl
44	449.5	72.9	297	2	US-09-486-814A-2	Sequence 2, Appli
45	448.5	72.7	453	2	US-09-301-593-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-814-806-4
; Sequence 4, Application US/0814806
; Patent No. 5986065
GENERAL INFORMATION:
 ; APPLICANT: Wong, Hing C.
 ; APPLICANT: Jiao, Jin-an
 ; APPLICANT: Esperanza, Nieves
 ; APPLICANT: Lawrence, Luepschen
 ; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
 ; TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/814,806
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Corless, Peter F
 ; REGISTRATION NUMBER: 33,860
 ; REFERENCE/DOCKET NUMBER: 46943
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 117 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:

US-08-814-806-4

Query Match   99.8%;   Score 616;   DB 1;   Length 117;
Best Local Similarity 100.0%;   Pred. No. 2.9e-52;
Matches 117; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 2
US-09-293-854-4
; Sequence 4, Application US/09293854
; Patent No. 6555319
; GENERAL INFORMATION:
;   APPLICANT: Wong, Hing C.
;   Jiao, Jin-an
;   Esperanza, Nieves
;   Lawrence, Luepschen
;   TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
;   COAGULATION AND METHODS OF USE THEREOF
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;   STREET: 130 Water Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/293,854
;   FILING DATE: 16-Apr-1999
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/814,806
;   FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Corless, Peter F
;   REGISTRATION NUMBER: 33,860
;   REFERENCE/DOCKET NUMBER: 46943
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-523-3400
;   TELEFAX: 617-523-6440
;   TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO:4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: N-terminal
;   ORIGINAL SOURCE:
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-293-854-4

Query Match   99.8%;   Score 616;   DB 2;   Length 117;
Best Local Similarity 100.0%;   Pred. No. 2.9e-52;
Matches 117; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Db   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 3
US-09-647-468-139
; Sequence 139, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
;   APPLICANT: SATO, KOH
;   APPLICANT: ADACHI, HIDEKI
;   APPLICANT: YABUTA, NAOHIRO
;   TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;   TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;   FILE REFERENCE: 053466/0289
;   CURRENT APPLICATION NUMBER: US/09/647,468
;   CURRENT FILING DATE: 2000-09-29
;   PRIOR APPLICATION NUMBER: PCT/JP99/01768
;   PRIOR FILING DATE: 1999-04-02
;   PRIOR APPLICATION NUMBER: JP 10-91850
;   PRIOR FILING DATE: 1998-04-03
;   NUMBER OF SEQ ID NOS: 183
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF
;   OTHER INFORMATION: mouse monoclonal antibody ATR-2
; US-09-647-468-139

Query Match   84.5%;   Score 521.5;   DB 2;   Length 118;
Best Local Similarity 83.9%;   Pred. No. 3.9e-43;
Matches   99; Conservative   8; Mismatches   10; Indels   1; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          ||||||||||||||||||||||||||:||:||||:||:||||||||||||||||||||||
Db   1 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
          ||||||||||||||||||||||||||:::||:||||:| :|:||||||||||||||||
Db   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSEDSAVYYCARGEGYYFDYWGQGTTLTVSS 118

RESULT 4
US-09-647-468-140
; Sequence 140, Application US/09547468
; Patent No. 6677436
; GENERAL INFORMATION:
;   APPLICANT: SATO, KOH
;   APPLICANT: ADACHI, HIDEKI
;   APPLICANT: YABUTA, NAOHIRO
;   TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;   TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;   FILE REFERENCE: 053466/0289
;   CURRENT APPLICATION NUMBER: US/09/647,468
;   CURRENT FILING DATE: 2000-09-29
;   PRIOR APPLICATION NUMBER: PCT/JP99/01768
;   PRIOR FILING DATE: 1999-04-02
;   PRIOR APPLICATION NUMBER: JP 10-91850
;   PRIOR FILING DATE: 1998-04-03
;   NUMBER OF SEQ ID NOS: 183
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 140
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:

; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-140

Query Match   84.5%;   Score 521.5;   DB 2;   Length 118;
Best Local Similarity   83.9%;   Pred. No. 3.9e-43;
Matches   99;   Conservative   8;   Mismatches   10;   Indels   1;   Gaps   1;

Qy   1   EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
       ||||||||||||||||||||:|||| |||||:|||||:|||||||||||||| ||
Db   1   EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60

Qy   61   DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
       :|||||||||||||||||||||||||||:||| :||||||||||||
Db   61   NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGEGYYFDYWGQGTTLTVSS 118

RESULT 5
US-09-647-468-153
; Sequence 153, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 153
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for H chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-153

Query Match   84.5%;   Score 521.5;   DB 2;   Length 137;
Best Local Similarity   83.9%;   Pred. No. 4.6e-43;
Matches   99;   Conservative   8;   Mismatches   10;   Indels   10;   Gaps   1;

Qy   1   EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
       ||||||||||||||||||||:|||| |||||:|||||:|||||||||||||| ||
Db   20   EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 79

Qy   61   DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
       :|||||||||||||||||||||||||||:||| :||||||||||||
Db   80   NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGEGYYFDYWGQGTTLTVSS 137

RESULT 6
US-09-647-468-154
; Sequence 154, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for H chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-154

Query Match   84.5%;   Score 521.5;   DB 2;   Length 137;
Best Local Similarity   83.9%;   Pred. No. 4.6e-43;
Matches   99;   Conservative   8;   Mismatches   10;   Indels   1;   Gaps   1;

Qy   1   EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
       ||||||||||||||||||||:|||| |||||:|||||:|||||||||||||| ||
Db   20   EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 79

Qy   61   DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
       :|||||||||||||||||||||||||||:||| :||||||||||||
Db   80   NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGEGYYFDYWGQGTTLTVSS 137

RESULT 7
US-08-273-146-55
; Sequence 55, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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;   MOLECULE TYPE: protein
US-08-273-146-55

Query Match             78.5%;  Score 484.5;  DB 1;  Length 116;
Best Local Similarity   76.1%;  Pred. No. 1.4e-39;
Matches   89;  Conservative   15;  Mismatches   12;  Indels   1;  Gaps   1;

Qy    1  EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY  60
         ::|||||||||||||||| ||:|:|:||:|:|||||||||||||:|:
Db    1  QVQLQQSGPELVKPGASVKVSCKASGYAFTNYNIYWVKQSHGKSLEWIGYIDPYSGGGSSY 60

Qy   61  DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS      117
         |||||||||||||||||||||||||:||| :|||:
Db   61  NQKFKGKATLTVDKSSSTAYMHLNSLTSEDSAVYYCAGG-NPRFAFWGQGTTVTVSS     116
```

RESULT 8
US-09-647-468-144
; Sequence 144, Application US/09647468
; Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 144
LENGTH: 118
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF mouse
OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-144

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Query Match             77.6%;  Score 478.5;  DB 2;  Length 118;
Best Local Similarity   76.3%;  Pred. No. 5.5e-39;
Matches   90;  Conservative   12;  Mismatches   15;  Indels   1;  Gaps   1;

Qy    1  EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY  60
         :|||||||||||||||||||:|:||:||:|||||||||||||:|:|
Db    1  DIQLQQSGPELVKPGASVKVSCKASGYSFTDYNIFWFKQSHGKSLEWIGYIDPYTGGTGY  60

Qy   61  DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALD-FWGQGTTLTVSS     117
         |||||||||||||||||||||||||:||| :|||:
Db   61  NQKFNDKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGFYYDYCYWGQGTLVTVSA     118
```

RESULT 9
US-09-647-468-158
; Sequence 158, Application US/09647468
; Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 158
LENGTH: 137
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: sequence coding for H chain V region of anc-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-158

```
Query Match             77.6%;  Score 478.5;  DB 2;  Length 137;
Best Local Similarity   76.3%;  Pred. No. 6.5e-39;
Matches   90;  Conservative   12;  Mismatches   15;  Indels   1;  Gaps   1;

Qy    1  EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY  60
         :|||||||||||||||||||:|:||:||:|:|||||||||||||:|:|
Db   20  DIQLQQSGPELVKPGASVKVSCKASGYSFTDYNIFWVKQSHGKSLEWIGYIDPYTGGTGY  79

Qy   61  DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALD-FWGQGTTLTVSS     117
         :|||||||||||||||||||||||||:||| :|||:
Db   80  NQKFNDKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGFYYDYCYWGQGTLVTVSA     137
```

RESULT 10
US-08-672-345C-105
; Sequence 105, Application US/08672345C
; Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-672-345C-105

```
Query Match             76.7%;  Score 473.5;  DB 1;  Length 116;
Best Local Similarity   75.2%;  Pred. No. 1.6e-38;
Matches   88;  Conservative   13;  Mismatches   15;  Indels   1;  Gaps   1;

Qy    1  EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY  60
         ||||||||||||||||| :|:|:||:||:|:|||||||||||||:|:
Db    1  EIHLQQSGPELVKPGASVKLSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPHNGGIFY  60
```

```
Qy   61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
             :||||:|||||||||  ||||||||||||||   :|||  :|||
Db   61  NQKFKGRATLTVDKSSNTAFMHLNSLTSEDSAVYYCARG-GGLFAYWGRGTLVTVSA 116
```

RESULT 11
US-09-214-095D-90
; Sequence 90, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-90

Query Match   76.7%; Score 473.5; DB 2; Length 116;
Best Local Similarity 75.2%; Pred. No. 1.6e-38;
Matches 88; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

```
Qy    1  EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
            ||||||||||||||||:||:||  ||||||||||||||||||||||||||||:||
Db    1  EIHLQQSGPELVKPGASVKLSCKASGYSFTDYNMWVKQSHGKSLEWIGYIDPHNGGIFY 60

Qy   61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
            :||||:|||||||||  ||||||||||||||   :|||  :|||
Db   61  NQKFKGRATLTVDKSSNTAFMHLNSLTSEDSAVYYCARG-GGLFAYWGRGTLVTVSA 116
```

RESULT 12
US-09-940-727B-90
; Sequence 90, Application US/09940727B
; Patent No. 6913917
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 116
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-90

Query Match   76.7%; Score 473.5; DB 2; Length 116;
Best Local Similarity 75.2%; Pred. No. 1.6e-38;
Matches 88; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

```
Qy    1  EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
            ||||||||||||||||:||:||  ||||||||||||||||||||||||||||:||
Db    1  EIHLQQSGPELVKPGASVKLSCKASGYSFTDYNMWVKQSHGKSLEWIGYIDPHNGGIFY 60

Qy   61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
            :||||:|||||||||:|:||||||||||||||   :||:|||
Db   61  NQKFKGRATLTVDKSSNTAFMHLNSLTSEDSAVYYCARG-GGLFAYWGRGTLVTVSA 116
```

```
Qy   61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
            :||||:|||||||||  |||||||||:||||||||||   :||:|||
Db   61  NQKFKGKATLTVDKSSTTAYLELRSLTSEDTAVYFCARDHDYYFDFWGQGTLTVSS 117
```

RESULT 13
US-09-802-083-5
; Sequence 5, Application US/0980283
; Patent No. 6703494
; GENERAL INFORMATION:
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Lowe, David G.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced
; TITLE OF INVENTION: Anticoagulant Potency
; FILE REFERENCE: P1736R1
; CURRENT APPLICATION NUMBER: US/09/802,083
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-802-083-5

Query Match   76.5%; Score 472; DB 2; Length 118;
Best Local Similarity 75.2%; Pred. No. 2.3e-38;
Matches 88; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

```
Qy    1  EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
            |:|||||||||||||||||:||  |||:||||||||||||||||||:||||||||:||
Db    1  EVLLQQSGPELVKPGASVKIPCKASGYTFTEYNMDWVKQSHGKSLEWIGDINPNNGNTIY 60

Qy   61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
            :||||:|||||||||  |||||||||:||||||||||   :||:|||
Db   61  NQKFKGKATLTVDKSSTTAYLELRSLTSEDTAVYFCARDHDYYFDFWGQGTLTVSS 117
```

RESULT 14
US-09-647-468-143
; Sequence 143, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-143

Query Match   76.1%; Score 469.5; DB 2; Length 118;
Best Local Similarity 74.6%; Pred. No. 4e-38;
Matches 88; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

```
Qy    1  EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
            :||||||||||||||||:||:||  |||:||||||||||||||||||||||||||:||
Db    1  DIQLQQSGPELVKPGSSVKVSCKASGYSFPDYNIFWVKQSHGKSLEWIGYIDPYTGGTGY 60

Qy   61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALD-FWGQGTTLTVSS 117
```

```
Db               :|| |  ||||||||||||:||:||||||||||||||||||:|||||:|||      | :||||| :|||:
             61 NQKFNDKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGFYYDCYWGQGTLVTVSA 118


RESULT 15
US-09-647-468-157
; Sequence 157, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
;   APPLICANT: SATO, KOH
;   APPLICANT: ADACHI, HIDEKI
;   APPLICANT: YABUTA, NAOHIRO
;   TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;   TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;   FILE REFERENCE: 053466/0289
;   CURRENT APPLICATION NUMBER: US/09/647,468
;   CURRENT FILING DATE: 2000-09-29
;   PRIOR APPLICATION NUMBER: PCT/JP99/01768
;   PRIOR FILING DATE: 1999-04-02
;   PRIOR APPLICATION NUMBER: JP 10-91850
;   PRIOR FILING DATE: 1998-04-03
;   NUMBER OF SEQ ID NOS: 183
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
;   LENGTH: 137
;   TYPE: PRT
;   ORGANISM: Mus sp.
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence coding for H chain V region of ant-TF
;   OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-157

Query Match             76.1%;  Score 469.5;  DB 2;  Length 137;
Best Local Similarity   74.6%;  Pred. No. 4.8e-38;
Matches    88;  Conservative   13;  Mismatches   16;  Indels    1;  Gaps     1;

Qy     1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
           ||||||||||||||||:||: |||    ||| ||||:||:||||||||||||||| |:||
Db    20 DIQLQQSGPELVKPGSSVKVSCKASGYSFPDYNIFWVKQSHGKSLEWIGYIDPYTGGTGY 79

Qy    61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALD-FWGQGTTLTVSS 117
           :| ||||||||||||||||||||||||:||||||||:|||    :||||| :|||:
Db    80 NQKFNDKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGFYYDCYWGQGTLVTVSA 137


Search completed: April 18, 2006, 13:41:12
Job time : 48 secs
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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:      April 18, 2006, 13:35:55 ; Search time 39 Seconds
                                         (without alignments)
                                         288.650 Million cell updates/sec

Title:       US-10-764-140-4
Perfect score: 617
Sequence:    1 EIQLQQSGPELVKPGASVQV..........RDVTTALDFWGQGTTLTVSS 117

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
             1: piri:*
             2: pir2:*
             3: pir3:*
             4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	468.5	75.9	137	2	H32513	Ig heavy chain pre
2	465.4	75.4	139	2	A27609	Ig heavy chain pre
3	463	75.0	117	2	MHMS4E	Ig heavy chain V r
4	463	75.0	140	1	T01407	Ig heavy chain (my
5	461.5	74.8	128	2	I37267	Ig heavy chain V r
6	460	74.6	117	1	MHMSJ5	Ig heavy chain V r
7	452.5	73.3	119	2	F30502	Ig heavy chain pre
8	449	72.8	118	2	PL0200	anti-DNA autoantib
9	448.5	72.7	112	2	S09957	Ig heavy chain V-D
10	448	72.6	117	2	S03305	Ig heavy chain V r
11	446.5	72.4	120	2	A49982	Ig heavy chain V r
12	443	71.8	151	2	PL0011	Ig heavy chain pre
13	441.5	71.6	122	2	E37267	Ig heavy chain V r
14	441.5	71.6	128	2	C37267	Ig heavy chain V r
15	440	71.3	138	2	PH0105	anti-digoxin trans
16	439.5	71.2	135	2	PS0057	Ig heavy chain pre
17	438.5	71.1	114	2	S26319	Ig heavy chain V r
18	438	71.0	119	2	PH0099	Ig heavy chain V r
19	436	70.7	121	2	F37266	Ig heavy chain V r
20	435.5	70.6	469	2	S37483	Ig gamma-2a chain
21	433.5	70.3	118	1	MHMS38	Ig heavy chain V r
22	432	70.0	246	2	S38950	Ig gamma chain - m
23	432	70.0	446	2	S40295	Ig gamma-2a chain
24	429.5	69.6	122	2	PH0887	Ig heavy chain V r
25	429.5	69.6	128	2	A37267	Ig heavy chain V r
26	426.5	69.1	113	2	S55535	Ig heavy chain V r
27	426	69.0	166	2	PL0012	Ig heavy chain pre
28	425	68.9	121	2	H37266	Ig heavy chain V r
29	423.5	68.6	108	2	PH0975	Ig heavy chain V r
30	422	68.4	138	2	S45249	Ig heavy chain pre
31	421	68.2	117	2	S09961	Ig heavy chain V-D
32	421	68.2	119	2	B53285	Ig heavy chain V a
33	421	68.2	125	2	PH0100	Ig heavy chain V r
34	420.5	68.2	150	2	PN0444	Ig heavy chain V r
35	419.5	68.0	113	2	S55528	Ig heavy chain V r
36	419	67.9	116	2	S55542	Ig heavy chain V r
37	419	67.9	117	1	HVMS8A	Ig heavy chain pre
38	419	67.9	140	2	PH1482	Ig heavy chain V r
39	419	67.9	140	2	S04575	Ig heavy chain pre
40	418.5	67.8	131	2	S66537	Ig heavy chain V r
41	418	67.7	136	1	HVMSB1	Ig heavy chain pre
42	417.5	67.7	113	2	S55534	Ig heavy chain V r
43	417.5	67.7	117	2	S25176	Ig heavy chain V r
44	417.5	67.7	120	2	E45722	anti-glycoprotein
45	417	67.6	113	2	PH0974	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J.Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and
A;Reference number: A94689; MUID:88331394; PMID:3118286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Cross-references: UNIPARC:UPI000011409A; GB:M20831; NID:g196949; PIDN:AAA38848.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match       75.9%;    Score 468.5;  DB 2;    Length 137;
Best Local Similarity  75.4%;  Pred. No. 1.3e-35;
Matches   89;    Conservative  14;   Mismatches  14;   Indels  1;   Gaps  1;

Qy       1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWRQSHGKSLEWIGYIDPYNGITIY 60
           ||||||||||||||||||||| :|||||||||| :||:||||||||||||||||||||||
Db      20 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNINPYYGSTSY 79

Qy      61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
           :|||||||||||||||||| :|:|: |||||||||||| :|||||||||||||||||||
Db      80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARKNYGSSFDYWGQGTTLTVSS 137

RESULT 2
A27609
Ig heavy chain precursor V region (I29) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swi
A;Reference number: A27609; MUID:88154467; PMID:3126234
A;Accession: A27609
A;Molecule type: DNA
A;Residues: 1-139 <KLE>
A;Cross-references: UNIPARC:UPI0000114D5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; P
C;Genetics:
C;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F;34-117/Domain: immunoglobulin homology <IMM>
```

```
Query Match      75.4%;  Score 465.5;  DB 2;  Length 139;
Best Local Similarity   72.5%;  Pred. No. 2.4e-35;
Matches   87; Conservative   18; Mismatches   12; Indels    3; Gaps    1;

Qy     1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
         :|||||||||||||||||:|||||||::||:|||| ::||:||||||||||||:|||||
Db    20 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYVNHWVKQSNGKSLEWIGYINPYNDYTSY 79

Qy    61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR--DVTTALDFWGQGTTLTVSS 117
         :|||||||||||||| |||||::||||||||||:|| ||  ::||:||||:|||||||
Db    80 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARYSYYSYYAMDVWGQGTSVTVSS 139
```

RESULT 3
MHMS4E
Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Accession: A02039
R;Kehry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
Biochemistry 21, 5415-5424, 1982
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain co...
A;Reference number: A02039; MUID:83075344; PMID:6816276
A;Accession: A02039
A;Molecule type: protein
A;Residues: 1-117 <KEH>
A;Cross-references: UNIPROT:P01756; UNIPARC:UPI00000270F1
C;Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context a...
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted
F;55/Binding site: carbohydrate (Asn) (covalent) #status atypical

```
Query Match      75.0%;  Score 463;  DB 1;  Length 117;
Best Local Similarity   74.4%;  Pred. No. 3.4e-35;
Matches   87; Conservative   13; Mismatches   17; Indels    0; Gaps    0;

Qy     1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
         :|||||||||||||||||:|||||::||||||||||:|||||||||||||||:|||||
Db     1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy    61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
         :||||||||||||||| |||||::||||
Db    61 NQKFKGKATLTVDKSSTAYMQLNSLTSEDSAVYYCARYDWYFDVWGAGTTVTVSS 117
```

RESULT 4
T01407
Ig heavy chain (myeloma M104E) - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C;Accession: T01407
R;Takahashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamot...
Microbiol. Immunol. 36, 855-863, 1992
A;Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and...
A;Reference number: Z14317; MUID:93116638; PMID:1474935
A;Accession: T01407
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-140 <TAK>
A;Cross-references: UNIPARC:UPI000011B29E; EMBL:S51851; NID:g262657
C;Superfamily: immunoglobulin V region; immunoglobulin homology

```
Query Match      75.0%;  Score 463;  DB 2;  Length 140;
Best Local Similarity   74.4%;  Pred. No. 4.1e-35;
Matches   87; Conservative   13; Mismatches   17; Indels    0; Gaps    0;

Qy     1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
         :|||||||||||||||||:|||||::||||||||||:|||||||||||||||:|||||
Db    20 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 79
```

```
Qy    61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
         :||||||||||||||| |||||::|||| ||||:||||::||| |:|||||||||||||||
Db    80 NQKFKGKATLTVDKSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTTVTVSS 136
```

RESULT 5
I37267
Ig heavy chain V region (129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C;Accession: I37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of ant...
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: I37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
A;Cross-references: UNIPARC:UPI000176C52
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

```
Query Match      74.8%;  Score 461.5;  DB 2;  Length 128;
Best Local Similarity   71.5%;  Pred. No. 5.1e-35;
Matches   88; Conservative   17; Mismatches   11; Indels   11; Gaps    2;

Qy     2 IQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGIYIDPYNGITIYD 61
         :||||||||||||||:|||||:|||::||||||||||||||||||||:||||:|||||:
Db     6 VQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGGTSYN 65

Qy    62 QNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCA-RDVTTAL-----DFWGQGTTLT 114
         :||||||||||||::|:| |:|||||||||||| |  :|::||      |:|||||||
Db    66 QKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGLTTVVAKSYYFPYDWYGQGTTLT 125

Qy   115 VSS 117
         |||
Db   126 VSS 128
```

RESULT 6
MHMSJ5
Ig heavy chain V region (J558) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A26242
R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.
Nature 283, 35-40, 1980
A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements...
A;Reference number: A26242; MUID:80078170; PMID:6765983
A;Accession: A26242
A;Molecule type: protein
A;Residues: 1-117 <SCH>
A;Cross-references: UNIPROT:P01757; UNIPARC:UPI00000270F2
A;Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that s...
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

```
Query Match      74.6%;  Score 460;  DB 1;  Length 117;
Best Local Similarity   74.4%;  Pred. No. 6.3e-35;
Matches   87; Conservative   13; Mismatches   17; Indels    0; Gaps    0;

Qy     1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
         :|||||||||||||||||:|||||::||||||||||:|||||||||||||||:|||||
Db     1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy    61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
         :||||||||||||||| |||||::||||
Db    61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 79
```

Db   61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWYFDVWGAGTTVTVSS 117

RESULT 7
F30502
Ig heavy chain V region (A52) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: F30502
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: F30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <EIL>
A;Cross-references: UNIPARC:UPI0000176B33
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   73.3%; Score 452.5; DB 2; Length 119;
Best Local Similarity   73.1%; Pred. No. 3.1e-34;
Matches 87; Conservative 12; Mismatches 17; Indels 3; Gaps 1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
Db   1 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGKINPYYGSTSY 60

Qy   61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTA---LDFWGQGTTLTVS 116
Db   61 NQKFKGQATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGRLRRGGYFDYWGQGTTLTVS 119

RESULT 8
PL0200
anti-DNA autoantibody BV16-19, heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0200
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N
A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0200
A;Molecule type: mRNA
A;Residues: 1-118 <SMI>
A;Cross-references: UNIPARC:UPI0000113784; GB:X53641; NID:g50193; PIDN:CAA37692.1; PID:g
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;50-66/Region: complementarity-determining 2
F;99-110/Region: complementarity-determining 3
F;99-106/Region: D region
F;107-118/Region: JH region

Query Match   72.8%; Score 449; DB 2; Length 118;
Best Local Similarity   72.0%; Pred. No. 6.3e-34;
Matches 85; Conservative 14; Mismatches 15; Indels 4; Gaps 1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
Db   1 EIQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNINPYYGGTSY 60

Qy   61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTA---LDFWGQGTTLT 114
Db   61 NQQFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGITTSTRTWFAYWGQGTLVT 118

RESULT 9
S09957
Ig heavy chain V-D-J region (106-10E) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Accession: S09957
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodi
A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09957
A;Molecule type: mRNA
A;Residues: 1-112 <REI>
A;Cross-references: UNIPARC:UPI000011E5C; EMBL:X51845; NID:g55244; PIDN:CAA36138.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   72.7%; Score 448.5; DB 2; Length 112;
Best Local Similarity   72.6%; Pred. No. 6.7e-34;
Matches 85; Conservative 14; Mismatches 13; Indels 5; Gaps 1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
Db   1 EVQLQQSGPELVKSGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGRVNPSNGGTSY 60

Qy   61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
Db   61 NQKFKGKATLTVDKSLSTAYMQLNSLTSEDSAVYYCARG-----DYNGQGTTLTVSS 112

RESULT 10
S03305
Ig heavy chain V region (6B12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: JL0044; S05276, S03305
R;Van Cleave, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A;Title: Do antibodies recognize amino acid side chains of protein antigens independent
A;Reference number: JL0043; MUID:88258372; PMID:2455014
A;Accession: JL0044
A;Molecule type: mRNA
A;Residues: 1-117 <VAN>
A;Cross-references: UNIPARC:UPI0000176B56; EMBL:X12381
R;Metzger, D.W.
submitted to the EMBL Data Library, July 1988
A;Reference number: S05276
A;Accession: S05276
A;Molecule type: mRNA
A;Residues: 1-116, 'T' <MET>
A;Cross-references: UNIPARC:UPI000011SDB3; EMBL:X12381; NID:g52094; PIDN:CAA03939.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   72.6%; Score 448; DB 2; Length 117;
Best Local Similarity   72.6%; Pred. No. 7.7e-34;
Matches 85; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
Db   1 EVQLQQSGPEAGKPGASVKMSCKASGYTFTDYYINWVKQSHGKSLEWIGYYPNIDETAY 60

Qy   61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
Db   61 SQKFKGKATLTVDKSSTAMELRSLTSDDSAVYYCARRNNVFYDVWGQGTTLTVSS 117

RESULT 11
A49982
Ig heavy chain V region (BA7.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: A49982
R;Lin, C.; Kieber-Emmons, T.; Villalobos, T.; Wahlgren, C.; Foster, M.H.; Kleyman, T...

J. Biol. Chem. 269, 2805-2813, 1994
A;Title: Topology of an amiloride-binding protein.
A;Reference number: A49982; MUID:94132051; PMID:8300613
A;Accession: A49982
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-120 <LIN>
A;Cross-references: UNIPARC:UPI000011A4A4; GB:L24802; NID:g452096; PIDN:AAA98740.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match   72.4%; Score 446.5; DB 2; Length 120;
Best Local Similarity 68.9%; Pred. No. 1.1e-33;
Matches 84; Conservative 18; Mismatches 13; Indels 7; Gaps 2;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          :|||||||||||||||||||||::||| |||||||:|||||||||||||||||:
Db   1 EVQLQQSGPELVKPGASVKISCKASGYSF GYIHWVKQSHVKSLEWIGHISPYNGATTY 60

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR-----DVTTALDFWGQGTTLTV 115
         :||| |||||||||||||||||||||||::||||||| :|:|||||||||||||
Db   61 NQNFKDTASLTVDKSSTSAYMELHSLTSEDSAVYYCARFNYYGHYT--MDYWGQGTSVTV 118

Qy 116 SS 117
          ||
Db 119 SS 120

RESULT 13
E37267
Ig heavy chain V region (Py42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000

RESULT 12
PL0011
Ig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0011
R;Cheng,H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0011
A;Molecule type: mRNA
A;Residues: 1-151 <CHE>
A;Cross-references: UNIPARC:UPI0000176D36
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcho
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;118-125/Region: complementarity-determining 3
F;137-151/Domain: C region (fragment) #status predicted <COR>

Query Match   71.8%; Score 443; DB 2; Length 151;
Best Local Similarity 70.1%; Pred. No. 2.9e-33;
Matches 82; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          |:|||||||||||||||||::||| :||| |||||||:|||||||||||||||||||
Db   20 EVQLQQSGPELLKPGASVKISCKASGYTFTDYTMHWVKQSHGKSLEWIGGFDPNYDNTFY 79

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
         :: || |||||||||||||||||||||||||||||||:|||||||:|||||||:||
Db   80 NEKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYYCASYDYGALDYWGQGTSVTVSS 136

C;Accession: E37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: E37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <RUF>
A;Cross-references: UNIPARC:UPI0000176B3C
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match   71.6%; Score 441.5; DB 2; Length 122;
Best Local Similarity 69.7%; Pred. No. 3.1e-33;
Matches 83; Conservative 20; Mismatches 11; Indels 5; Gaps 2;

Qy   2 IQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIYD 61
         :|||||||||||||||||||||::|| |:|:||||||||||||||||||||||||:||
Db   6 VQLQQSGPELVKPGASVKISCKTFGYTFTEYTIHWMKQSHGKSLEWIGGINPNTGGTINN 65

Qy   62 QNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCA---RDVTTALDFWGQGTTLTVSS 117
          |:||||||||||||||||||||||||||||||||| |:|||||||||||||:|||
Db   66 QKFRGKATLTVDKSSSTAYMELRSLTSEDSAVYFCARRGREYT--MDYWGQGTSVTVSS 122

RESULT 14
C37267
Ig heavy chain V region (Py69) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C;Accession: C37267
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: C37267
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-128 <RUF>
A;Cross-references: UNIPARC:UPI0000176B3A
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>

Query Match   71.6%; Score 441.5; DB 2; Length 128;
Best Local Similarity 66.7%; Pred. No. 3.3e-33;
Matches 82; Conservative 19; Mismatches 15; Indels 7; Gaps 1;

Qy   2 IQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIYD 61
         :|||||||||||||||::|| |:|:||||||||||||||||||::||:: :|:
Db   6 VQLQQSGPELVKPGASMKISCKTSGYTFTEYTMWVKQSHGKSLEWIGRFNPNSGGSTYN 65

Qy   62 QNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARD------VTTALDFWGQGTTLT 114
          |:||||||||||||||||||||||||||||||||| ::|||||||||||||
Db   66 QKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGPYGNYYTSYFDYWGQGTTLT 125

Qy 115 VSS 117
         |||
Db 126 VSS 128

RESULT 15
PH0105
anti-digoxin transfectoma antibody light chain V region precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: PH0105
R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.
Mol. Immunol. 27, 901-909, 1990
A;Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain
A;Reference number: PH0105; MUID:91015092; PMID:2120577

A;Accession: PH0105
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <NEA>
A;Cross-references: UNIPARC:UPI0000115EC4; GB:X56622; GB:S44836; NID:g49875; PIDN:CAA39S
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match   71.3%; Score 440; DB 2; Length 138;
Best Local Similarity   68.9%; Pred. No. 4.9e-33;
Matches   82; Conservative   19; Mismatches   16; Indels   2; Gaps   1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          |:||||||||||||||||| ::|||:||:: ||||||||||||| ||:|:|
Db   20 EVQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGVTGY 79

Qy   61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTT--ALDFWGQGTTLTVSS 117
          :|||||||||||||||||:||:| ||||||||| |:|:|| ::||||
Db   80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWAMDYWGHGASVTVSS 138

Search completed: April 18, 2006, 13:40:18
Job time : 40 secs

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                    GenCore version 5.1.7
             Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:      April 18, 2006, 13:40:31 ; Search time 165 Seconds
                                         (without alignments)
                                         296.279 Million cell updates/sec

Title:       US-10-764-140-4
Perfect score: 617
Sequence:    1 EIQLQQSGPELVKPGASVQV.........RDVTTALDFWGQGTTLTVSS 117

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:     1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA Main:*
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             3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
             4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
             5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
             6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

             Pred. No. is the number of results predicted by chance to have a
             score greater than or equal to the score of the result being printed,
             and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	617	100.0	117	3	US-09-990-586-4	Sequence 4, Appli
2	617	100.0	117	4	US-10-310-113-4	Sequence 4, Appli
3	617	100.0	117	4	US-10-230-880-4	Sequence 4, Appli
4	616	99.8	117	3	US-09-293-854-4	Sequence 4, Appli
5	616	99.8	117	4	US-10-293-417-4	Sequence 4, Appli
6	616	99.8	117	5	US-10-764-140-4	Sequence 4, Appli
7	616	99.8	117	5	US-10-618-338-4	Sequence 4, Appli
8	521.5	84.5	118	4	US-10-462-062-139	Sequence 139, Appl
9	521.5	84.5	118	4	US-10-462-062-140	Sequence 140, App
10	521.5	84.5	137	4	US-10-462-062-153	Sequence 153, App
11	521.5	84.5	137	4	US-10-462-062-154	Sequence 154, App
12	511.5	82.9	120	4	US-10-372-719-2	Sequence 2, Appli
13	511.5	82.9	120	5	US-10-505-747-2	Sequence 2, Appli
14	493	79.9	117	4	US-10-223-880-2	Sequence 2, Appli
15	492	79.7	119	4	US-10-774-076-2	Sequence 2, Appli
16	492	79.7	138	4	US-10-774-076-9	Sequence 9, Appli
17	487	78.9	113	3	US-09-924-099-2	Sequence 2, Appli
18	487	78.9	236	5	US-10-879-994-6	Sequence 6, Appli
19	487	78.9	236	3	US-10-610-452-6	Sequence 6, Appli
20	487	78.9	237	3	US-09-924-099-9	Sequence 9, Appli
21	487	78.9	243	3	US-09-924-099-10	Sequence 10, Appl
22	479.5	77.7	467	5	US-10-500-696-2	Sequence 2, Appli
23	478.5	77.6	118	4	US-10-462-062-144	Sequence 144, App
24	478.5	77.6	137	4	US-10-462-062-158	Sequence 158, App
25	474.5	76.9	214	3	US-10-488-074-69	Sequence 69, Appl
26	473.5	76.7	116	3	US-09-940-727B-90	Sequence 90, Appl
27	472	76.5	118	3	US-09-802-083-5	Sequence 5, Appli
28	472	76.5	118	4	US-10-165-732A-5	Sequence 5, Appli
29	472	76.5	118	4	US-10-172-78B-5	Sequence 5, Appli
30	469.5	76.5	118	4	US-10-745-455-5	Sequence 5, Appli
31	469.5	76.1	118	4	US-10-462-062-143	Sequence 143, App
32	469.5	76.1	137	5	US-10-462-062-157	Sequence 157, App
33	469.5	76.1	214	4	US-10-488-074-67	Sequence 67, Appl
34	468.5	75.9	139	4	US-10-365-122-28	Sequence 28, Appl
35	468.5	75.9	214	5	US-10-488-074-71	Sequence 71, Appl
36	467.5	75.8	116	5	US-10-389-155-15	Sequence 15, Appl
37	467.5	75.8	116	4	US-10-389-417-15	Sequence 15, Appl
38	467.5	75.8	116	4	US-10-452-357-56	Sequence 56, Appl
39	467.5	75.8	135	5	US-10-389-155-60	Sequence 60, Appl
40	467.5	75.8	135	4	US-10-389-417-60	Sequence 60, Appl
41	467.5	75.8	135	4	US-10-452-357-69	Sequence 69, Appl
42	467.5	75.8	135	5	US-10-837-904-27	Sequence 27, Appl
43	467.5	75.8	139	4	US-10-687-035-34	Sequence 34, Appl
44	466	75.5	118	5	US-10-996-316-203	Sequence 203, App
45	465.5	75.4	116	3	US-09-940-727B-14	Sequence 14, Appl

ALIGNMENTS

```
RESULT 1
US-09-990-586-4
; Sequence 4, Application US/0990586
; Publication No. US2003010968OA1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 71758/46943-CIP2
; CURRENT APPLICATION NUMBER: US/09/990,586
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-586-4

  Query Match             100.0%;  Score 617;  DB 3;  Length 117;
  Best Local Similarity   99.1%;  Pred. No. 4.7e-52;
  Matches  116;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy      1 EIQLQQSGPELVKPGASVQVSCK(TX)QYSFTDYNVYWRQSHGKSLEWIGYIDPYNGITIY 60
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db      1 EIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWRQSHGKSLEWIGYIDPYNGITIY 60

Qy     61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 2
US-10-310-113-4
; Sequence 4, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
```

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;    PRIOR FILING DATE: 2001-11-21
;    PRIOR APPLICATION NUMBER: 60/343,306
;    PRIOR FILING DATE: 2001-10-29
;    PRIOR APPLICATION NUMBER: 09/293,854
;    PRIOR FILING DATE: 1999-04-16
;    PRIOR APPLICATION NUMBER: 08/814,806
;    PRIOR FILING DATE: 1997-03-10
;    NUMBER OF SEQ ID NOS: 169
;    SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 4
;    LENGTH: 117
;    TYPE: PRT
;    ORGANISM: Murine sp.
;  US-10-310-113-4

Query Match             100.0%;  Score 617;  DB 4;  Length 117;
Best Local Similarity    99.1%;  Pred. No. 4.7e-52;
Matches  116;  Conservative    0;  Mismatches    1;  Indels     0;  Gaps     0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 3
US-10-230-880-4
; Sequence 4, Application US/10230880
; Publication No. US2003019705A1
; GENERAL INFORMATION:
;    APPLICANT: WONG, HING C.
;    APPLICANT: STINSON, JEFFREY L.
;    APPLICANT: MOSQUERA, LUIS A.
;    TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
;    FILE REFERENCE: 71758/58066
;    CURRENT APPLICATION NUMBER: US/10/230,880
;    CURRENT FILING DATE: 2002-12-23
;    PRIOR APPLICATION NUMBER: 09/990,586
;    PRIOR FILING DATE: 2001-11-21
;    PRIOR APPLICATION NUMBER: 60/343,306
;    PRIOR FILING DATE: 2001-10-29
;    PRIOR APPLICATION NUMBER: 09/293,854
;    PRIOR FILING DATE: 1999-04-16
;    NUMBER OF SEQ ID NOS: 174
;    SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 4
;    LENGTH: 117
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;  US-10-230-880-4

Query Match             100.0%;  Score 617;  DB 4;  Length 117;
Best Local Similarity    99.1%;  Pred. No. 4.7e-52;
Matches  116;  Conservative    0;  Mismatches    1;  Indels     0;  Gaps     0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 4
US-09-293-854-4
; Sequence 4, Application US/09293854
; Patent No. US2002016357A1
; GENERAL INFORMATION:
;    APPLICANT: Wong, Hing C.
```

(second column)

```
;             Jiao, Jin-an
;             Esperanza, Nieves
;             Lawrence, Luepschen
;    TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
;             COAGULATION AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES: 26
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;       STREET: 130 Water Street
;       CITY: Boston
;       STATE: MA
;       COUNTRY: USA
;       ZIP: 02109
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette
;       COMPUTER: IBM Compatible
;       OPERATING SYSTEM: DOS
;       SOFTWARE: FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/293,854
;       FILING DATE: 16-Apr-1999
;       CLASSIFICATION: <Unknown>
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/814,806
;       FILING DATE: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Corless, Peter F
;       REGISTRATION NUMBER: 33,860
;       REFERENCE/DOCKET NUMBER: 46943
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 617-523-3400
;       TELEFAX: 617-523-6440
;       TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 4:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 117 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;    MOLECULE TYPE: peptide
;    HYPOTHETICAL: NO
;    ANTI-SENSE: NO
;    FRAGMENT TYPE: N-terminal
;    ORIGINAL SOURCE:
;    SEQUENCE DESCRIPTION: SEQ ID NO: 4:
;  US-09-293-854-4

Query Match              99.8%;  Score 616;  DB 3;  Length 117;
Best Local Similarity   100.0%;  Pred. No. 5.9e-52;
Matches  117;  Conservative    0;  Mismatches    0;  Indels     0;  Gaps     0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 5
US-10-293-417-4
; Sequence 4, Application US/10293417
; Publication No. US2003008263A1
; GENERAL INFORMATION:
;    APPLICANT: Wong, Hing C.
;             Jiao, Jin-an
;             Esperanza, Nieves
;             Lawrence, Luepschen
;    TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
;             COAGULATION AND METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES: 26
;    CORRESPONDENCE ADDRESS:
```

```
;     ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;     STREET: 130 Water Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/293,417
;     FILING DATE: 12-No. US20030082636A1-2002
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/293,854
;     FILING DATE: 16-Apr-1999
;     APPLICATION NUMBER: 08/814,806
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Corless, Peter F
;     REGISTRATION NUMBER: 33,860
;     REFERENCE/DOCKET NUMBER: 46943
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-523-3400
;     TELEFAX: 617-523-6440
;     TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 117 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: N-terminal
;     ORIGINAL SOURCE:
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-293-417-4

Query Match    99.8%;  Score 616;  DB 4;  Length 117;
Best Local Similarity  100.0%;  Pred. No. 5.9e-52;
Matches 117;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1  EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy  61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117


RESULT 6
US-10-764-140-4
; Sequence 4, Application US/10764140
; Publication No. US20040229282A1
; GENERAL INFORMATION:
;   APPLICANT: WONG, HING C.
;   APPLICANT: JIAO, JIN-AN
;   TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
;   TITLE OF INVENTION:  OF USE THEREOF
;   FILE REFERENCE: 59918 (71758)
;   CURRENT APPLICATION NUMBER: US/10/764,140
;   CURRENT FILING DATE: 2004-01-22
;   PRIOR APPLICATION NUMBER: 10/293,417
;   PRIOR FILING DATE: 2002-11-12
;   PRIOR APPLICATION NUMBER: 09/293,854
;   PRIOR FILING DATE: 2002-04-16
;   PRIOR APPLICATION NUMBER: 08/814,806
;   PRIOR FILING DATE: 2002-03-10
```

```
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn Ver. 3.2
;
; SEQ ID NO 4
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (25)
;   OTHER INFORMATION: Variable amino acid
US-10-764-140-4

Query Match    99.8%;  Score 616;  DB 5;  Length 117;
Best Local Similarity  100.0%;  Pred. No. 5.9e-52;
Matches 117;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   1  EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy  61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117


RESULT 7
US-10-618-338-4
; Sequence 4, Application US/10618338
; Publication No. US20050089929A1
; GENERAL INFORMATION:
;   APPLICANT: Wong, Hing C.
;             Jiao, Jin-an
;             Esperanza, Nieves
;             Lawrence, Luepschen
;   TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
;                       COAGULATION AND METHODS OF USE THEREOF
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;     STREET: 130 Water Street
;     CITY: Boston
;     STATE: MA
;     COUNTRY: USA
;     ZIP: 02109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/618,338
;     FILING DATE: 11-Jul-2003
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/293,854
;     FILING DATE: 16-Apr-1999
;     APPLICATION NUMBER: 08/814,806
;     FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Corless, Peter F
;     REGISTRATION NUMBER: 33,860
;     REFERENCE/DOCKET NUMBER: 46943
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 617-523-3400
;     TELEFAX: 617-523-6440
;     TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 117 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide
```

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;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       FRAGMENT TYPE: N-terminal
;       ORIGINAL SOURCE:
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-618-338-4

Query Match             99.8%;  Score 616;  DB 5;  Length 117;
Best Local Similarity   100.0%; Pred. No. 5.9e-52;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

RESULT 8
US-10-462-062-139
; Sequence 139, Application US/10462062
; Publication No. US2004044187A1
; GENERAL INFORMATION:
;       APPLICANT: SATO, KOH
;       APPLICANT: ADACHI, HIDEKI
;       TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
;       TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;       FILE REFERENCE: 053466-0360
;       CURRENT APPLICATION NUMBER: US/10/462,062
;       CURRENT FILING DATE: 2003-06-16
;       PRIOR APPLICATION NUMBER: PCT/JP99/01768
;       PRIOR FILING DATE: 1999-04-02
;       PRIOR APPLICATION NUMBER: JP 10-91850
;       PRIOR FILING DATE: 1998-04-03
;       NUMBER OF SEQ ID NOS: 183
;       SOFTWARE: PatentIn Ver. 2.1
;       SEQ ID NO 139
;       LENGTH: 118
;       TYPE: PRT
;       ORGANISM: Artificial Sequence
;       FEATURE:
;       OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of
;       OTHER INFORMATION: H chain V region of anti TF mouse monoclonal antibody ATR-2
US-10-462-062-139

Query Match             84.5%;  Score 521.5;  DB 4;  Length 118;
Best Local Similarity   83.9%;  Pred. No. 8.6e-43;
Matches 99; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              ||||||||||||||||||||||||||||| |||:||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
              ||||||||||||||||||:|||||||||||||||||| :||||||||||||||||||
Db         61 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGEGYYFDYWGQGTTLTVSS 118

RESULT 9
US-10-462-062-140
; Sequence 140, Application US/10462062
; Publication No. US2004044187A1
; GENERAL INFORMATION:
;       APPLICANT: SATO, KOH
;       APPLICANT: ADACHI, HIDEKI
;       TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
;       TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;       FILE REFERENCE: 053466-0360
;       CURRENT APPLICATION NUMBER: US/10/462,062
;       CURRENT FILING DATE: 2003-06-16
;       PRIOR APPLICATION NUMBER: PCT/JP99/01768
;       PRIOR FILING DATE: 1999-04-02
;       PRIOR APPLICATION NUMBER: JP 10-91850
;       PRIOR FILING DATE: 1998-04-03
;       NUMBER OF SEQ ID NOS: 183
;       SOFTWARE: PatentIn Ver. 2.1
;       SEQ ID NO 140
;       LENGTH: 118
;       TYPE: PRT
;       ORGANISM: Artificial Sequence
;       FEATURE:
;       OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of
;       OTHER INFORMATION: H chain V region of anti TF mouse monoclonal antibody ATR-3
US-10-462-062-140

Query Match             84.5%;  Score 521.5;  DB 4;  Length 118;
Best Local Similarity   83.9%;  Pred. No. 8.6e-43;
Matches 99; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              ||||||||||||||||||||||||||||| |||:||||||||||||||||||||||||||
Db          1 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
              |||||||||||||||||| :||||||||||||||||| :||||||||||||||||||
Db         61 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGEGYYFDYWGQGTTLTVSS 118

RESULT 10
US-10-462-062-153
; Sequence 153, Application US/10462062
; Publication No. US2004044187A1
; GENERAL INFORMATION:
;       APPLICANT: SATO, KOH
;       APPLICANT: ADACHI, HIDEKI
;       TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
;       TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;       FILE REFERENCE: 053466-0360
;       CURRENT APPLICATION NUMBER: US/10/462,062
;       CURRENT FILING DATE: 2003-06-16
;       PRIOR APPLICATION NUMBER: PCT/JP99/01768
;       PRIOR FILING DATE: 1999-04-02
;       PRIOR APPLICATION NUMBER: JP 10-91850
;       PRIOR FILING DATE: 1998-04-03
;       NUMBER OF SEQ ID NOS: 183
;       SOFTWARE: PatentIn Ver. 2.1
;       SEQ ID NO 153
;       LENGTH: 137
;       TYPE: PRT
;       ORGANISM: Artificial Sequence
;       FEATURE:
;       OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
;       OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
;       OTHER INFORMATION: antibody ATR-2
US-10-462-062-153

Query Match             84.5%;  Score 521.5;  DB 4;  Length 137;
Best Local Similarity   83.9%;  Pred. No. 1e-42;
Matches 99; Conservative 8; Mismatches 10; Indels 1; Gaps 1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              ||||||||||||||||||||||||||||| |||:||||||||||||||||||||||||||
Db         20 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 79

Qy         61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
              ||||||||||||||||||:|||||||||||||||||| :||||||||||||||||||
Db         80 NQKFKGKATLTVDKSSSTAFMHLNSLTSEDSAVYYCARGGEGYYFDYWGQGTTLTVSS 137

RESULT 11
US-10-462-062-154
; Sequence 154, Application US/10462062
; Publication No. US2004044187A1
; GENERAL INFORMATION:
```

```
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 154
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for H chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-3
US-10-462-062-154

  Query Match             84.5%;  Score 521.5;  DB 4;  Length 137;
  Best Local Similarity   83.9%;  Pred. No. 1e-42;
  Matches   99;  Conservative    8;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                 ||||||||||||||||| :|||  |||| |||||  ||:|||||||||||||||||:|
Db         20 EIQLQQSGPELVKPGASVKVSCKASGYSF TDYNMWVKQSHGKSLEWIGYIDPYNGGTIY 79

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
              :| ||||||||||||||| |||||||||||:|||| :||   ::|||||||||||||
Db         80 NQKFKGKATLTVDKSSTAFMHLNSLTSEDSAVYYCARGGEGYFDYWGQGTTLTVSS 137


RESULT 12
US-10-372-719-2
; Sequence 2, Application US/10372719
; Publication No. US2004005643A1
; GENERAL INFORMATION:
; APPLICANT: DE SANTIS, RITA
; APPLICANT: ANASTASI, ANNA MARIA
; TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY
; FILE REFERENCE: 2818-141
; CURRENT APPLICATION NUMBER: US/10/372,719
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 60/359,299
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: ST2146 heavy chain variable region protein sequence
US-10-372-719-2

  Query Match             82.9%;  Score 511.5;  DB 4;  Length 120;
  Best Local Similarity   76.7%;  Pred. No. 8.2e-42;
  Matches   92;  Conservative   17;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                 ||||||||||||||||| :||||   ||||| ||:|||||||||||||||||:|
Db          1 KVKLQQSGPELVKPGASVKVSCKASGYAFTSYNMYWVKQSHGKSLEWIGYIDPYNGVTSY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR---DVTTALDFWGQGTTLTVSS 117
              :| |||||||||||||| |||||||||||:|||| :|||      :|||||||||:|||
Db         61 NQKFKGKATLTVDKSSTAYMHLNSLTSEDSAVYYCARGGGSIYYAMDYWGQGTTVTVSS 120
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RESULT 13
US-10-505-747-2
; Sequence 2, Application US/10505747
; Publication No. US2005010614 5A1
; GENERAL INFORMATION:
; APPLICANT: DE SANTIS, RITA
; APPLICANT: ANASTASI, ANNA MARIA
; TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY
; FILE REFERENCE: 2818-141
; CURRENT APPLICATION NUMBER: US/10/505,747
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: 60/359,299
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: ST2146 heavy chain variable region protein sequence
US-10-505-747-2

  Query Match             82.9%;  Score 511.5;  DB 5;  Length 120;
  Best Local Similarity   76.7%;  Pred. No. 8.2e-42;
  Matches   92;  Conservative   17;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                 ||||||||||||||||| :||||   ||||| ||:|||||||||||||||||:|
Db          1 KVKLQQSGPELVKPGASVKVSCKASGYAFTSYNMYWVKQSHGKSLEWIGYIDPYNGVTSY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR---DVTTALDFWGQGTTLTVSS 117
              :| |||||||||||||| |||||||||||:|||| :|||      :|||||||||:|||
Db         61 NQKFKGKATLTVDKSSTAYMHLNSLTSEDSAVYYCARGGGSIYYAMDYWGQGTTVTVSS 120


RESULT 14
US-10-223-880-2
; Sequence 2, Application US/10223880
; Publication No. US20030152571A1
; GENERAL INFORMATION:
; APPLICANT: JONAK, ZDENKA
; APPLICANT: JOHANSON, KYUNG O.
; APPLICANT: TAYLOR, ALEXANDER
; TITLE OF INVENTION: ANIT-ALPHABETA3 HUMANIZED MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: P50629C1
; CURRENT APPLICATION NUMBER: US/10/223,880
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 09/380,910
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/04987
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/039,609
; PRIOR FILING DATE: 1997-03-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-223-880-2

  Query Match             79.9%;  Score 493;  DB 4;  Length 117;
  Best Local Similarity   76.1%;  Pred. No. 4.9e-40;
  Matches   89;  Conservative   15;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                 ||||||||||||||||| :||||   ||||| ||:|||||||||||||||||:|
Db          1 EIQLQQSGPEVVKPGASVKVSCKASGYAFTSYNMWVKQSHGKSLEWIGYIDPYNGDTFY 60

Qy         61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
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Db          :| |||||||||||||:||:||||||||||:|||::|||         :|||||:|||:
         61 NQKPFKGKATLTVDKSSSTAYMHLNSLTSEDSAVFYCARQNYGSFAYWGQGTLVTVSA 117


RESULT 15
US-10-774-076-2
; Sequence 2, Application US/10774076
; Publication No. US20040210040A1
; GENERAL INFORMATION:
;   APPLICANT: Protein Design Labs, Inc.
;   APPLICANT: Landolfi, et al.
;   TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
;   TITLE OF INVENTION: Psoriasis
;   FILE REFERENCE: 05882.0064.NPUS01
;   CURRENT APPLICATION NUMBER: US/10/774,076
;   CURRENT FILING DATE: 2004-02-06
;   NUMBER OF SEQ ID NOS: 39
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: mus sp.
US-10-774-076-2

Query Match             79.7%;  Score 492;  DB 4;  Length 119;
Best Local Similarity   78.2%;  Pred. No. 6.3e-40;
Matches   93; Conservative  11; Mismatches  13; Indels   2; Gaps   1;

Qy    1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
          |||||||||||||||:|||:||||| |||:|:: ||:|||||||||||||||||||| |
Db    1 EIQLQQSGPELVKPGASVKVSCKASGYAFTNYNMYWVKQSHGKSLEWIGYIDPYYGDPGY 60

Qy   61 DQNFKGKATLTVDKSSTAFMHLNSLTSDDSAVYFCAR--DVTTALDFWGQGTTLTVSS 117
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Search completed: April 18, 2006, 13:44:03
Job time : 166 secs
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                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

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Title:         US-10-764-140-1
Perfect score: 321
Sequence:      1 gacattcagatgaccagtc........ggaccaagctggagctgaaa 321

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5883141 seqs, 2842172653 residues

Total number of hits satisfying chosen parameters:    11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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                2: gb_in:*
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                4: gb_om:*
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                6: gb_pat:*
                7: gb_ph:*
                8: gb_pr:*
                9: gb_ro:*
               10: gb_sts:*
               11: gb_sy:*
               12: gb_un:*
               13: gb_vi:*
               14: gb_htg:*
               15: gb_pl:*

SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	321	100.0	321	6	AR087417	AR087417 Sequence
2	321	100.0	321	6	BD057834	BD057834 Antibodie
3	321	100.0	321	6	AR308506	AR308506 Sequence
4	293.8	91.5	375	6	AR452626	AR452626 Sequence
5	293.8	91.5	375	6	AR452627	AR452627 Sequence
6	291.4	90.8	318	9	MMY13991	Y13991 Mus musculu
7	290.6	90.5	321	9	MMALCVR25	X90900 M.musculus
8	289.4	90.2	324	9	MUSIGKADP	M36760 Mouse Ig re
9	288.8	90.0	324	9	MUSIGKADN	M36758 Mouse Ig re
10	287.4	89.5	1135	9	AX100597	AX100597 Sequence
11	287.4	89.5	1135	11	AF302092	AF302092 Synthetic
12	287.2	89.5	324	9	MUSIGKADO	M36759 Mouse Ig re
13	287	89.4	1228	6	E10065	E10065 Synthetic D
14	287	89.4	1228	6	I72625	I72625 Sequence 35
15	287	89.4	1300	6	E10064	E10064 Synthetic D
16	287	89.4	1300	6	I72624	I72624 Sequence 34
17	286.6	89.3	318	9	MMY13992	Y13992 Mus musculu
18	286	89.1	330	9	MMU557029	AJ557029 Mus muscu

19	282.6	88.0	324	9	AF030230	AF030230 Mus muscu
20	282	87.9	318	9	MUSIGKADQ	M36761 Mouse Ig re
21	277.4	86.4	295	6	E10043	E10043 cDNA's enco
22	277.4	86.4	295	6	I72603	I72603 Sequence 4
23	275.6	85.9	627	9	MMU235949	AJ235949 Mus muscu
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27	239.4	74.6	321	6	BD222154	BD222154 Immunolog
28	239.4	74.6	321	6	AX006748	AX006748 Sequence
29	239.4	74.6	362	11	AY648681	AY648681 Mus muscu
30	239.4	74.6	366	6	AR220107	AR220107 Sequence
31	239.4	74.6	366	6	AR220108	AR220108 Sequence
32	239.4	74.6	366	6	AR369279	AR369279 Sequence
33	239.4	74.6	366	6	AR369280	AR369280 Sequence
34	239.4	74.6	366	6	AR476745	AR476745 Sequence
35	239.4	74.6	366	6	AR476746	AR476746 Sequence
36	239.4	74.6	366	6	AR478142	AR478142 Sequence
37	239.4	74.6	366	6	AR478143	AR478143 Sequence
38	239.4	74.6	724	6	AR403540	AR403540 Sequence
39	239.4	74.6	864	11	XXU34924	U34924 Synthetic r
40	237.8	74.1	381	9	MUSIGKMADQ	L24555 Mus musculu
41	237.6	74.0	303	9	MUSIGKAAAK	M57988 Mouse IgK C
42	236.4	73.6	269	9	MUSIGKADL	M36756 Mouse Ig re
43	236.2	73.6	364	9	AY208327	AY208327 Mus muscu
44	236.2	73.6	366	6	AR220109	AR220109 Sequence
45	236.2	73.6	366	6	AR369281	AR369281 Sequence

ALIGNMENTS

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RESULT 1
AR087417
LOCUS       AR087417                 321 bp    DNA        linear    PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5986065.
ACCESSION   AR087417
VERSION     AR087417.1  GI:10014180
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Wong,H.C., Jiao,J.-A., Nieves,E.Liliana. and Luepschen,L.
  TITLE     Antibodies for inhibiting blood coagulation and methods of use
            thereof
  JOURNAL   Patent: US 5986065-A 1 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1..321
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Query Match             100.0%;  Score 321;  DB 6;  Length 321;
Best Local Similarity   100.0%;  Pred. No. 8.8e-88;
Matches  321;  Conservative   0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          1 GACATTCAGATGACCCAGTCTCCTGCCTCCCTGTCTGCATCTCGGGAGAAAGTGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATTCAGATGACCCAGTCTCCTGCCTCCCTGTCTGCATCTCGGGAGAAAGTGTCACC 60

Qy         61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db         61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy        121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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Db        121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy        181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
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Db        181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
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DEFINITION   Sequence 1 from patent US 6555319.
ACCESSION   AR308506
VERSION   AR308506.1 GI:31699968
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 321)
AUTHORS   Wong,H.C., Jiao,J.-A., Nieves,E.L. and Luepschen,L.
TITLE   Antibodies for inhibiting blood coagulation and methods of use
              thereof
JOURNAL   Patent: US 6555319-A 1 29-APR-2003;
              Sunol Molecular Corporation; Miramar, FL
FEATURES   Location/Qualifiers
     source   1..321
              /organism="unknown"
              /mol_type="mRNA"
ORIGIN

Query Match   100.0%; Score 321; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 8.8e-88;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCGCCTCCCAGTCTGCCATCTCTGGGAGAAAGTGTCACC 60
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Db   1 GACATTCAGATGACCCAGTCTCCGCCTCCCAGTCTGCCATCTCTGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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Db 121 GGGAAATCTCCTCAGCTCCTGATTTATGTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy 181 AGGTTCAGTGGCAGTGGGATCTGGGACACAAATTTCTTTCCAAGATCAGCAGCCTACAGGCT 240
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Db 181 AGGTTCAGTGGCAGTGGGATCTGGGACACAAATTTCTTTCCAAGATCAGCAGCCTACAGGCT 240

Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy 301 GGGACCAAGCTGGAGCTGAAA 321
        |||||||||||||||||||||
Db 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 4
AR452626
LOCUS   AR452626   375 bp DNA   linear PAT 20-FEB-2004
DEFINITION   Sequence 12 from patent US 6677436.
ACCESSION   AR452626
VERSION   AR452626.1 GI:42684507
KEYWORDS   .
SOURCE   Unknown.
ORGANISM   Unknown.
              Unclassified.
REFERENCE   1 (bases 1 to 375)
AUTHORS   Sato,K., Adachi,H. and Yabuta,N.
TITLE   Humanized antibody against human tissue factor (TF) and process of
              production of the humanized antibody
JOURNAL   Patent: US 6677436-A 12 13-JAN-2004;
              Chugai Seiyaku Kabushiki Kaisha; Tokyo;
              JPX;
FEATURES   Location/Qualifiers
     source   1..375
              /organism="unknown"
              /mol_type="genomic DNA"
ORIGIN

Query Match   91.5%; Score 293.8; DB 6; Length 375;
Best Local Similarity 94.7%; Pred. No. 2.2e-79;

Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy 301 GGGACCAAGCTGGAGCTGAAA 321
        |||||||||||||||||||||
Db 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 2
BD057834
LOCUS   BD057834   321 bp DNA   linear PAT 27-AUG-2002
DEFINITION   Antibodies for inhibiting blood coagulation and methods of use
              thereof.
ACCESSION   BD057834
VERSION   BD057834.1 GI:22603440
KEYWORDS   JP 200151621-A/1.
SOURCE   synthetic construct
ORGANISM   synthetic construct
              other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 321)
AUTHORS   Wong,H.C., Jiao,J.-A., Nieves,E.L. and Luepschen,L.
TITLE   Antibodies for inhibiting blood coagulation and methods of use
JOURNAL   Patent: JP 200151621-A 1 25-SEP-2001;
              SUNOL MOLECULAR CORP
COMMENT   PN   JP 200151621-A/1
              PD   25-SEP-2001
              PF   10-MAR-1998 JP 1998539703
              PI   HING C WONG,JIN AN JIAO,ESPERANZA LILIANA NIEVES,LAWRENCE
              PI   LUEPSCHEN
              PC   C07K16/00,C07K16/28,C07K16/18,C12N15/12,C12N15/13,A61K39/395
              CC   Strandedness: Single;
              CC   Topology: Linear;
              FH   Key   Location/Qualifiers
FEATURES   source   1..321
                       /organism="synthetic construct"
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ORIGIN

Query Match   100.0%; Score 321; DB 6; Length 321;
Best Local Similarity 100.0%; Pred. No. 8.8e-88;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCGCCTCCCAGTCTGCCATCTCTGGGGAGAAAGTGTCACC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GACATTCAGATGACCCAGTCTCCGCCTCCCAGTCTGCCATCTCTGGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCCTCCCTCAGCTCCTGATTTATGTGCTGCCACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db   61 ATCACATGCCTCCCTCAGCTCCTGATTTATGTGCTGCCACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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Db 181 AGGTTCAGTGGCAGTGGGATCTGGGACACAAATTTCTTTCCAAGATCAGCAGCCTACAGGCT 240

Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy 301 GGGACCAAGCTGGAGCTGAAA 321
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Db 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 3
AR308506
LOCUS   AR308506   321 bp mRNA   linear PAT 12-JUN-2003

Matches   304; Conservative   0; Mismatches   17; Indels   0; Gaps   0;

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Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTGTGGGAGAAAGTGTCACC    60
          ||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db     55 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTGTGGGAGAAAGTGTCACC   114

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACACATGGTTAGCATGGTATCAGCAGAAACCA   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 ATCACATGCCTGGCAAGTCAGACCATTGGTATCAGCAGAAACCA   174

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA   180
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    175 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA   234

Qy    181 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT   240
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Qy    241 GAAGATTTTGTAAATATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT   300
          |||||||||| |||| |||||||||||||||||||||||| ||| ||||||||||||||
Db    295 GAAGATTTTGTAAGTATTATTACTGTCAACAACTTTACAGTACTCCGTACACGTTCGGAGGG   354

Qy    301 GGGACCAAGCTGGAGCTGAAA   321
          ||||||||||||||| | |||
Db    355 GGGACCAAGCTGGAAATAAAA   375
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RESULT 5
AR452627
LOCUS       AR452627                375 bp    DNA        linear        PAT 20-FEB-2004
DEFINITION  Sequence 13 from patent US 6677436.
ACCESSION   AR452627
VERSION     AR452627.1  GI:42684508
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Sato,K., Adachi,H. and Yabuta,N.
  TITLE     Humanized antibody against human tissue factor (TF) and process of
            production of the humanized antibody
  JOURNAL   Patent: US 6677436-A 13 13-JAN-2004;
            Chugai Seiyaku Kabushiki Kaisha; Tokyo;
            JPX;
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ORIGIN
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Query Match   91.5%; Score 293.8; DB 6; Length 375;
Best Local Similarity 94.7%; Pred. No. 2.2e-79;
Matches 304; Conservative   0; Mismatches   17; Indels   0; Gaps   0;

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Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTGTGGGAGAAAGTGTCACC    60
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Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACACATGGTTAGCATGGTATCAGCAGAAACCA   120
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Db    115 ATCACATGCCTGGCAAGTCAGACCATTGGTATCAGCAGAAACCA   174

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA   180
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Qy    181 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT   240
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Db    235 AGGTTCAGTGGCAGTGGTAGTGGATCGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT   294

Qy    241 GAAGATTTTGTAAATATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT   300
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Db    295 GAAGATTTTGTAAGTATTATTACTGTCAACAACTTTACAGTACTCCGTACACGTTCGGAGGG   354
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Qy    301 GGGACCAAGCTGGAGCTGAAA   321
          ||||||||||||||| | |||
Db    355 GGGACCAAGCTGGAAATAAAA   375

RESULT 6
MMY13991
LOCUS       MMY13991                318 bp    mRNA        linear        ROD 14-APR-2000
DEFINITION  Mus musculus mRNA for immunoglobulin VK domain of anti-viral
            haemorrhagic septicaemia virus, clone 3F1H10.
ACCESSION   Y13991
VERSION     Y13991.1  GI:222725
KEYWORDS    immunoglobulin; kappa chain; light chain; variable region.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 318)
  AUTHORS   Lorenzen,N., Olesen,N.J. and Jorgensen,P.E.
  TITLE     Neutralization of Egtved virus pathogenicity to cell cultures and
            fish by monoclonal antibodies to the viral G protein
  JOURNAL   J. Gen. Virol. 71 (Pt 3), 561-567 (1990)
   PUBMED   1690259
REFERENCE   2
  AUTHORS   Lorenzen,N., Cupit,P.M., Secombes,C.J. and Cunningham,C.
  TITLE     Three monoclonal antibodies to the VHS virus glycoprotein:
            comparison of reactivity in relation to differences in
            immunoglobulin variable domain gene sequences
  JOURNAL   Fish Shellfish Immunol. 10 (2), 129-142 (2000)
   PUBMED   1038729
REFERENCE   3  (bases 1 to 318)
  AUTHORS   Cupit,P.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-1997) Cupit P.M., Molecular and Cell Biology,
            University of Aberdeen, Institute of Medical Science, Foresterhill,
            Aberdeen, AB15 2ZD SCOTLAND, UK
FEATURES             Location/Qualifiers
     source          1..318
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                     /db_xref="taxon:10090"
                     /clone="3F1H10"
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                     /protein_id="CAA74324.1"
                     /db_xref="GI:222726"
                     /translation="DIQMTQSPASQSASLGESVTTCLASQTIGTWLAWYQQKGKSP
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                     /evidence=experimental
ORIGIN
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Query Match   90.8%; Score 291.4; DB 9; Length 318;
Best Local Similarity 95.0%; Pred. No. 1.2e-78;
Matches 301; Conservative   0; Mismatches   16; Indels   0; Gaps   0;

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Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTCGCATCTCTGGGAGAAAGTGTCACC    60
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Db      1 GACATTCAGATGATGACCCAGTCTCCTGCCTCCCAGTCTCGCATCTCTGGGAGAAAGTGTCACC    60

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACCATTGATACAGTTAGCATGGTATCAGCAGAAACCA   120
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     61 ATCACATGCCTGGCAAGTCAGACCATTGGTATCAGCAGAAACCA   120

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA   180
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCAACCAGTTTGCAGATGGGGTCCCATCA   180
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Left column (RESULT 7)

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Qy  181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Db  181 AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy  241 GAAGATTTGTAAATTATTACTGTCAACAAGTTTCAGTTCTCCATTCACGTTCGGTGCT 300
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Db  241 GAAGATTTGTAAGTTATTACTGTCAACAACTTTCAGTTCTCCATTCACGTTCGGTCGGTGCT 300

Qy  301 GGGACCAAGTGGAGCT 317
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Db  301 GGGACCAAGTCGAGAT 317
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RESULT 7
MMALCVR25
LOCUS   MMALCVR25   321 bp   DNA   linear   ROD 31-AUG-1996
DEFINITION M.musculus antibody light chain variable region (321bp).
ACCESSION   X90900
VERSION   X90900.1 GI:1518326
KEYWORDS   antibody light chain; variable region.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Geiser,M. and Kretzschmar,T.
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 321)
  AUTHORS   Geiser,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-AUG-1995) M. Geiser, CIBA-GEIGY LTD, CDDT,
            K-681.5.46, CH-4002, Basel, SWITZERLAND
FEATURES   Location/Qualifiers
     source   1..321
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                     /mol_type="genomic DNA"
                     /strain="BALB/c"
                     /db_xref="taxon:10090"
                     /cell_type="lymphocytes"
                     /tissue_type="spleen"
                     /dev_stage="12 weeks old"
     CDS   <1..>321
                     /codon_start=1
                     /product="antibody light chain variable region"
                     /protein_id="CAA62408.1"
                     /db_xref="GI:1518327"
                     /translation="DIQMTQTPASQSASLGESVTITCLASQTIGTWLAWYQQIPGKSP
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                     KLEIK"
ORIGIN

Query Match   90.5%; Score 290.6; DB 9; Length 321;
  Best Local Similarity 94.1%; Pred. No. 2.2e-78;
  Matches 302; Conservative   0; Mismatches 19; Indels   0; Gaps   0;

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Qy    1 GACATTCAGATGACGCAGTCTCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
            ||||||||||| |||   ||| |||||||||||||||||||||||||||||||||| ||||||||
Db    1 GACATTCAGATGACGACGCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAAGTGTCACC 60

Qy   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGATACCA 120

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTGGCAGATGGGGTCCCATCA 180
            |||||||||||||||||||||||||||||||| |  ||| |||||||||||||||||
Db  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCAACCAGCTTGGCAGATGGGGTCCCATCA 180

Qy  181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
            ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Right column (RESULT 8)

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Qy  241 GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db  241 GAAGATTTGTAAGTTATTACTGTCAACAACTTTACAGTCAGTCAGTACTCCGTGGACGTTCGGTGGG 300

Qy  301 GGGACCAAGTGGAGCTGAAA 321
            || |||||| |||||   ||
Db  301 GGCACCAAGCTGGAAATCAAA 321
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RESULT 8
MUSIGKADP
LOCUS   MUSIGKADP   324 bp   mRNA   linear   ROD 27-APR-1993
DEFINITION Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds.
ACCESSION   M36760
VERSION   M36760.1 GI:196619
KEYWORDS   J-region; V-region; immunoglobulin light chain; processed gene.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 324)
  AUTHORS   Clarke,S., Rickert,R., Wloch,M.K., Staudt,L., Gerhard,W. and
            Weigert,M.
  TITLE   The BALB/c secondary response to the Sb site of influenza virus
            hemagglutinin. Nonrandom silent mutation and unequal numbers of VH
            and Vk mutations.
  JOURNAL   J. Immunol. 145 (7), 2286-2296 (1990)
  PUBMED   2398280
COMMENT   Original source text: Mouse (strain Balb/c), cDNA to mRNA,
            anti-influenza hemagglutinin hybridoma H37-92 Vk.
            Draft entry and computer-readable sequence for [J. Immunol. (1990)
            In press] kindly submitted
            by S.H.Clarke, 18-JUL-1990.
FEATURES   Location/Qualifiers
     source   1..324
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
     CDS   <1..>324
                     /note="Ig kappa-chain V-J-region"
                     /codon_start=1
                     /protein_id="AAA38757.1"
                     /db_xref="GI:196620"
                     /translation="DIQMTQSPXSQSASLGESVTITCLASQTIGTWLAWYQQKPGKSP
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                     XLEIKR"
ORIGIN   Chromosome 6.

Query Match   90.2%; Score 289.4; DB 9; Length 324;
  Best Local Similarity 93.1%; Pred. No. 5.1e-78;
  Matches 299; Conservative   0; Mismatches 22; Indels   0; Gaps   0;

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Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCCTCTGGGAGAAAGTGTCACC 60
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Db    1 GACATTCAGATGACCCAGTCTCCTNCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCAACTTGGCAGATGGGGTCCCATCA 180
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Db  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCAACCAGCTTGGCAGATGGGGTCCCATCA 180

Qy  181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Db  181 AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTCTTTCAAGATCANCANNNCCTACAGGCT 240

Qy  241 GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
            |||||||||||| |||||||||||||||| |||||||| ||||   ||||||||| ||
Db  241 GAAGATTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTGGACGTTCGGTGA 300
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Right column

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Qy  301 GGGACCAAGCTGGAGCTGAAA 321
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Db  301 GGGACCAANGCTGGAAATCAAA 321
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RESULT 10
AX100597
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LOCUS       AX100597               1135 bp    DNA     linear   PAT 10-APR-2001
DEFINITION  Sequence 1 from Patent WO0121800.
ACCESSION   AX100597
VERSION     AX100597.1  GI:13619600
KEYWORDS    
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Secombes,C.J., Cunningham,C. and Lorenzen,N.
  TITLE     Monoclonal antibody 3f1h10 neutralising vhsv (viral haemorrhagic
            septicaemia virus)
  JOURNAL   Patent: WO 0121800-A 1 29-MAR-2001;
            ABERDEEN UNIVERSITY (GB) ; Statens Veterinaere Serumlaboratorium
            (DK)
FEATURES             Location/Qualifiers
     source          1..1135
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence:single chain
                     antibody gene (BU1) inserted into E. coli pCDNA3 plasmid
                     (Invitorgen)"
ORIGIN

Query Match             89.5%;  Score 287.4;  DB 6;  Length 1135;
Best Local Similarity   93.5%;  Pred. No. 1.9e-77;
Matches  300;  Conservative  0;  Mismatches  21;  Indels  0;  Gaps  0;

Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db  478 GACATCGAGCTCACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 537

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db  538 ATCACATGCCTGGCAAGTCAGACCAGACATTGGTACATGGTTAGCATGGTATCAACAGAAACCA 597

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACAAATTTCTTCAAGATGGGGTCCCATCA 180
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Db  598 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACAAACCAGTTTGGCAGATGGGGTCCCATCA 657

Qy  181 AGGTTCAGTGGCAGTGGATCTGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
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Db  658 AGGTTCAGTGGCAGTGGATCTGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 717

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCCATTCACGTTCGGTGCT 300
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Db  718 GAAGATTTTGTAAGTTATTACTGTCAACAACTTACAGTACTCCGTACACGTTCGGAGGG 777

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
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Db  778 GGGACCAAGCTGGAGATCAAA 798
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RESULT 11
AF302092
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LOCUS       AF302092               1135 bp    DNA     linear   SYN 26-SEP-2002
DEFINITION  Synthetic construct single chain antibody BU1 gene, complete cds.
ACCESSION   AF302092
VERSION     AF302092.1  GI:11162742
KEYWORDS    
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Lorenzen,N., Cupit,P.M., Einer-Jensen,K., Lorenzen,E., Ahrens,P.,
            Secombes,C.J. and Cunningham,C.
  TITLE     Immunoprophylaxis in fish by injection of mouse antibody genes
  JOURNAL   Nat. Biotechnol. 18 (11), 1177-1180 (2000)
  PUBMED    11062437
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Left column

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Qy  301 GGGACCAAGCTGGAGCTGAAA 321
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Db  301 GGCACCAAGGCTGGAAATCAAA 321
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RESULT 9
MUSIGKADN
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LOCUS       MUSIGKADN               324 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds.
ACCESSION   M36758
VERSION     M36758.1  GI:196615
KEYWORDS    J-region; V-region; immunoglobulin light chain; processed gene.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Clarke,S., Rickert,R., Wloch,M.K., Staudt,L., Gerhard,W. and
            Weigert,M.
  TITLE     The BALB/c secondary response to the Sb site of influenza virus
            hemagglutinin. Nonrandom silent mutation and unequal numbers of VH
            and Vk mutations
  JOURNAL   J. Immunol. 145 (7), 2286-2296 (1990)
  PUBMED    2398280
  COMMENT   Original source text: Mouse (strain Balb/c), cDNA to mRNA,
            anti-influenza hemagglutinin hybridoma H37-54 Vk.
            Draft entry and computer-readable sequence for [J. Immunol. (1990)
            In press] kindly submitted
            by S.H.Clarke,18-JUL-1990.
FEATURES             Location/Qualifiers
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                     RLEIKR"
ORIGIN      Chromosome 6.

Query Match             90.0%;  Score 288.8;  DB 9;  Length 324;
Best Local Similarity   93.1%;  Pred. No. 7.8e-78;
Matches  299;  Conservative  0;  Mismatches  22;  Indels  0;  Gaps  0;

Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
        |||| ||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    1 GACATTCAGATGACCCAGTCTCCTTNCCTCCCAGTCTGCATCTCTGGCATCTCTGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db   61 ATCACATGCCTGGCAAGTCAGACCAGACCAGGTTAGCATGGTATCAGCAGAAACCA 120

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACAAACTTGGCAGATGGGGTCCCATCA 180
        ||||||||||||||||||||||||||||||||||||||    |||||||||||||||||||
Db  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACAAACCAGTTTGGCAGATGGGGTCCCATCA 180

Qy  181 AGGTTCAGTGGCAGTGGATCTGGCATCGGCAACCAGGCTGCCAGCAGGGGTCCAGGCT 240
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Db  181 AGGTTCAGTGGCAGTGGATCTGGCATCGGCACAAAATTTCTTCAAGATCANNNNCCTACAGGCT 240

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAGTTTCAATTTTCATTCACGTTCGGTGCT 300
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Db  241 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTGACGTTCGGTGGA 300

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REFERENCE   2 (bases 1 to 1135)
AUTHORS   Ahrens,P. and Cupit,P.
TITLE   Direct Submission
JOURNAL   Submitted (01-SEP-2000) Fish Section, Danish Veterinary Laboratory,
            Hangovej 2, Aarhus DK-8200, Denmark
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     CDS   13..1122
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                     /transl_table=11
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                     /protein_id="AAG39978.1"
                     /db_xref="GI:11692741"
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     misc_feature   1126..1135
                     /note="derived from Invitrogen pCDNA3"
ORIGIN

Query Match   89.5%; Score 287.4; DB 11; Length 1135;
Best Local Similarity   93.5%; Pred. No. 1.9e-77;
Matches 300; Conservative   0; Mismatches 21; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   478 GACATTCAGAGTCACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 537

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db   538 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAACAGAAACCA 597

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   598 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCAACCAGTTGGCAGATGGGGTCCCATCA 657

Qy   181 AGGTTCAGTGGCAGTGGATCTGGGACAACTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
           ||||||||||||||||||||||||| |||||||||||||||||||||||||| |||||
Db   658 AGGTTCAGTGGTAGTGGATCTGGGACACAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 717

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   718 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTTCCGTACAGTTCGGAGGG 777

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
           ||||| |||||||||||| |||
Db   778 GGGACCAAGCTGGAGATCAAA 798

RESULT 12
MUSIGKADO
LOCUS   MUSIGKADO   324 bp   mRNA   linear   ROD 27-APR-1993
DEFINITION Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds.
ACCESSION   M36759
VERSION   M36759.1 GI:196617
KEYWORDS   J-region; V-region; immunoglobulin light chain; processed gene.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 324)
  AUTHORS   Clarke,S., Rickert,R., Wloch,M.K., Staudt,L., Gerhard,W. and

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TITLE   Weigert,M.
            The BALB/c secondary response to the Sb site of influenza virus
            hemagglutinin. Nonrandom silent mutation and unequal numbers of VH
            and Vk mutations
JOURNAL   J. Immunol. 145 (7), 2286-2296 (1990)
PUBMED   2398280
COMMENT   Original source text: Mouse (strain Balb/c), cDNA to mRNA,
            anti-influenza hemagglutinin hybridoma H37-50 Vk.
            Draft entry and computer-readable sequence for [J. Immunol. (1990)
            In press] kindly submitted
            by S.H.Clarke, 18-JUL-1990.
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
     CDS   <1..>324
                     /note="Ig kappa-chain V-J-region"
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                     /db_xref="GI:196618"
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                     RLEIKR"
ORIGIN   Chromosome 6.

Query Match   89.5%; Score 287.2; DB 9; Length 324;
Best Local Similarity   92.8%; Pred. No. 2.4e-77;
Matches 299; Conservative   0; Mismatches 23; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db   61 NTCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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Db   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGGACAACTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
           ||||||||||||| |||||||||||||||||| ||||||| |||||||||| ||||| |
Db   241 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTTCCGTGGACGTTCGGTGGA 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
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Db   301 GGGACCAGCTGGAAATCAAA 321

RESULT 13
E10065
LOCUS   E10065   1228 bp   DNA   linear   PAT 29-SEP-1997
DEFINITION Synthetic DNA fragments.
ACCESSION   E10065
VERSION   E10065.1 GI:22026691
KEYWORDS   JP 195265077-A/24.
SOURCE   unidentified
  ORGANISM unidentified
            unclassified.
REFERENCE   1 (bases 1 to 1228)
  AUTHORS   Okuno,Y., Oshima,A., Yoshioka,H., Takahata,T. and Katou,I.
  TITLE   DNA CODING FOR ANTIBODY VARIABLE REGION
  JOURNAL   Patent: JP 195265077-A 24 17-OCT-1995;
            TAKARA SHUZO CO LTD
COMMENT   OS   None
            OC   Artificial sequences.
            PN   JP 195265077-A/24

Query Match   89.4%;   Score 287;   DB 6;   Length 1228;
Best Local Similarity   93.7%;   Pred. No. 2.5e-77;
Matches 299;   Conservative   0;   Mismatches   20;   Indels   0;   Gaps   0;

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Db    517  GACATCGAGCTCACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC  576

Qy     61  ATCACATGCCTGGCAAGTCAGACCAGACCATTGATACATGGTTAGCATGGTATCAGAGAAACCA  120
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    577  ATCACATGCCTGGCAAGTCAGACCATTGGTACATGGTTAGCATGGTATCAGCAGAAACCA  636

Qy    121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
           |||||||||||||||||||||||||||||||||||  |||| ||||||||||||||||||
Db    637  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCAACCAGCTTGGCAGATGGGGTCCCATCA  696

Qy    181  AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT  240
           |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db    697  AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTCCTTCAAGATCAGCAGCCTACAGGCT  756

Qy    241  GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTTCCATTCACGTTCGGTGCT  300
           ||||||||||| |||| ||||||||||||||||||||||||| ||| |||||||||||
Db    757  GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTGACGTTCGGTGGA  816

Qy    301  GGGACCAAGCTGGAGCTGA  319
           || |||||||||||| ||
Db    817  GGCACCAAGCTGGAGTCGA  835
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RESULT 15
E10064
LOCUS   E10064   1300 bp   DNA   linear   PAT 29-SEP-1997
DEFINITION   Synthetic DNA fragments.
ACCESSION   E10064
VERSION   E10064.1   GI:22026690
KEYWORDS   JP 199265077-A/23.
SOURCE   unidentified
  ORGANISM   unidentified
             unclassified.
REFERENCE   1 (bases 1 to 1300)
  AUTHORS   Okuno,Y., Oshima,A., Yoshioka,H., Takahata,T. and Katou,I.
  TITLE   DNA CODING FOR ANTIBODY VARIABLE REGION
  JOURNAL   Patent: JP 199265077-A 23 17-OCT-1995;
             TAKARA SHUZO CO LTD
COMMENT   OS   None
             OC   Artificial sequences.
             PN   JP 199265077-A/23
             PD   17-OCT-1995
             PF   30-MAR-1994 JP 1994082693
             PI   OKUNO YOSHINOBU, OSHIMA ATSUSHI, YOSHIOKA HIROFUMI, PI
             TAKAHATA TAKASHI,
             PI   KATOU IKUNOSHIN
             PC   C12N15/09//A61K39/145,C07K16/10,C12N1/21,C12P21/08,G01N33/53,
             PC   G01N33/569,
             PC   G01N33/577,(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12P21/08,PC
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             CC   strandedness: Single;
             CC   topology: Linear;
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ORIGIN
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Query Match    89.4%;    Score 287;    DB 6;    Length 1228;
Best Local Similarity    93.7%;    Pred. No. 2.5e-77;
Matches 299;    Conservative    0;    Mismatches    20;    Indels    0;    Gaps    0;

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Qy      1  GACATTCAGATGACCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60
           |||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db    517  GACATCGAGCTCACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC  576

Qy     61  ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGAGAAACCA  120
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Db    577  ATCACATGCCTGGCAAGTCAGACCATTGGTACATGGTTAGCATGGTATCAGCAGAAACCA  636

Qy    121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
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Db    637  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCAACCAGCTTGGCAGATGGGGTCCCATCA  696

Qy    181  AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT  240
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Db    697  AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTCCTTCAAGATCAGCAGCCTACAGGCT  756

Qy    241  GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTTCCATTCACGTTCGGTGCT  300
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Db    757  GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGGGACGTTCGGTGGA  816

Qy    301  GGGACCAAGCTGGAGCTGA  319
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Db    817  GGCACCAAGCTGGAGTCGA  835
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RESULT 14
I72625
LOCUS   I72625   1228 bp   DNA   linear   PAT 03-APR-1998
DEFINITION   Sequence 35 from patent US 5684146.
ACCESSION   I72625
VERSION   I72625.1   GI:3008764
KEYWORDS   .
SOURCE   Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE   1 (bases 1 to 1228)
  AUTHORS   Okuno,Y., Oshima,A., Yoshioka,H., Takabatake,T. and Kato,I.
  TITLE   DNA coding for variable region to human influenza A type virus
  JOURNAL   Patent: US 5684146-A 35 04-NOV-1997;
FEATURES   Location/Qualifiers
     source   1..1228
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ORIGIN

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Query Match          89.4%;  Score 287; DB 6;  Length 1300;
Best Local Similarity  93.7%;  Pred. No. 2.5e-77;
Matches  299;  Conservative   0;  Mismatches  20;  Indels   0;  Gaps   0;

Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC  60
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Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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Db  709 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCAACCAGCTTGGCAGATGGGGTCCCATCA 768

Qy  181 AGGTTCAGTGGCAGTGGATCTGGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Db  769 AGGTTCAGTGGTAGTGGATCTGGGCACAAAATTTCCTTCAAGATCAGCAGCCTACAGGCT 828

Qy  241 GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
        |||||||||||||||| |||||||||||||| ||||| | ||||||||||||| ||||||||||
Db  829 GAAGATTTTGTAAGTTATTATTACTGTCAACAACTTTACAGTACTCCGTGACGTTCGGTGGA 888

Qy  301 GGGACCAAGCTGGAGCTGA 319
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Db  889 GGCACCAAGCTGGAGTCGA 907
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Search completed: April 18, 2006, 19:05:23
Job time : 2419 secs

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                 GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:     April 18, 2006, 18:23:59 ; Search time 456 Seconds
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Title:      US-10-764-140-1
Perfect score: 321
Sequence:   1 gacattcagatgacccagtc.........ggaccaagctggagctgaaa 321

Scoring table: IDENTITY_NUC
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Searched:   4996997 seqs, 333336308 residues

Total number of hits satisfying chosen parameters:       9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	321	100.0	321	2	AAV54961	Aav54961 Human ant
2	321	100.0	321	12	ADL35002	Adl35002 Murine an
3	321	100.0	321	13	ADU06807	Adu06807 Murine H3
4	321	100.0	321	14	ADW07325	Adw07325 Mouse ant
5	321	100.0	321	14	ADZ40936	Adz40936 H36.D2.B7
6	310	96.6	322	9	ACC58568	Acc58568 Anti-tiss
7	293.8	91.5	375	2	AAZ33012	Aaz33012 Anti-tiss
8	292.2	91.0	375	2	AAZ33013	Aaz33013 Anti-tiss
9	289	90.0	949	14	ADZ51613	Adz51613 High-func
10	287.4	89.5	1135	4	AAF76338	Aaf76338 Anti-VHSV
11	287	89.4	1300	14	AAT04179	Aat04179 C179Fv-PP
12	285.8	89.0	949	14	ADZ51605	Adz51605 High-func
13	285.4	88.9	1228	14	AAT04180	Aat04180 scFv-PP c
14	284.2	88.5	324	3	AAK99183	Aak99183 324nt DNA
15	282.6	88.0	949	14	ADZ51609	Adz51609 High-func
16	281	87.5	949	14	ADZ51611	Adz51611 High-func
17	281	87.5	949	14	ADZ51615	Adz51615 High-func
18	279.4	87.0	949	14	ADZ51607	Adz51607 High-func
19	278.4	86.7	312	2	AAQ41257	Aaq41257 c23.5 VL
20	275.8	85.9	295	2	AAT04160	Aat04160 Anti-huma
21	239.4	74.6	321	3	AAZ88324	Aaz88324 Anti-zeta
22	239.4	74.6	366	2	AAD27166	Aad27166 Single ch
23	239.4	74.6	366	2	AAD27165	Aad27165 Single ch
24	239.4	74.6	366	4	AAD21541	Aad21541 Single ch
25	239.4	74.6	366	4	AAD21540	Aad21540 Single ch
26	239.4	74.6	366	6	ABS53655	Abs53655 Anti-T-ce
27	239.4	74.6	366	6	ABS53654	Abs53654 Anti-T-ce
28	239.4	74.6	366	12	ADJ88101	Adj88101 Wild type
29	239.4	74.6	366	12	ADJ88102	Adj88102 Single ch
30	239.4	74.6	366	13	ADR03283	Adr03283 DNA encod
31	239.4	74.6	366	13	ADR03284	Adr03284 DNA encod
32	239.4	74.6	367	2	AAX87211	Aax87211 scFv-KJ16
33	239.4	74.6	367	2	AAX87210	Aax87210 Wild-type
34	239.4	74.6	724	2	AAX90423	Aax90423 Chimeric
35	236.2	73.6	366	2	AAD27167	Aad27167 Single ch
36	236.2	73.6	366	4	AAD21542	Aad21542 Single ch
37	236.2	73.6	366	6	ABS53656	Abs53656 Anti-T-ce
38	236.2	73.6	366	12	ADJ88103	Adj88103 Single ch
39	236.2	73.6	366	13	ADR03285	Adr03285 DNA encod
40	236.2	73.6	367	2	AAX87212	Aax87212 scFv-KJ16
41	236.2	73.6	1637	3	AAZ88358	Aaz88358 Bispecifi
42	233	72.6	1574	3	AAZ57599	Aaz57599 Erythrocy
43	231.4	72.1	324	2	AAA99634	Aaa99634 Rat antib
44	231.4	72.1	384	10	ADB97811	Adb97811 HEV relat
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ALIGNMENTS

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AAV54961
ID   AAV54961 standard; cDNA; 321 BP.
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AC   AAV54961;
XX
DT   10-DEC-1998  (first entry)
XX
DE   Human anti-tissue factor light chain variable region encoding cDNA.
XX
KW   Human; anti-tissue factor light chain variable region; H36.D2.B7;
KW   anti-tissue factor heavy chain variable region; inhibition; antibody;
KW   blood coagulation; thrombosis; restenosis; thromboembolic condition;
KW   cardiovascular; infection; neoplastic disease; clot; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key              Location/Qualifiers
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FT                    /tag=  a
FT                    /product= "anti-tissue factor light chain variable
FT                    region"
FT                    /note= "no stop codon given"
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PN   WO9840408-A1.
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PD   17-SEP-1998.
XX
PF   10-MAR-1998;  98WO-US004644.
XX
PR   10-MAR-1997;  97US-00814806.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Wong HC, Jiao J, Nieves EL, Luepschen L;
XX
DR   WPI; 1998-520804/44.
DR   P-PSDB; AAW71287.
XX
PT   New antibody to human tissue factor - used for, e.g. treating thrombosis
PT   or restenosis or thromboembolic conditions associated with
PT   cardiovascular, infectious or neoplastic disease.
```

```
XX
PS     Claim 11; Fig 1A; 53pp; English.
XX
CC     The present sequence encodes the human anti-tissue factor light chain
CC     variable region from an antibody that binds native human tissue factor
CC     (TF) and does not bind non-native TF. The antibody capable of
CC     specifically binding native TF may be used for inhibiting blood
CC     coagulation and also for reducing TF levels in a mammal. The antibodies
CC     can be used, e.g. to treat thromboses, particularly to prevent or inhibit
CC     restenosis, or other thromboses following an invasive medical procedure
CC     such as arterial or cardiac surgery (e.g. angioplasty, endarterectomy,
CC     deployment of a stent, use of catheter, graft implantation or use of an
CC     arteriovenous shunt). The antibodies can also be used as a carrier for
CC     drugs, particularly pharmaceuticals targeted for interaction with a blood
CC     clot such as streptokinase, tissue plasminogen activator (t-PA) or
CC     urokinase, or a cytotoxic agent by conjugating a suitable toxin to the
CC     antibody. Further the antibodies can be used for treating a
CC     thromboembolic condition associated with cardiovascular disease, an
CC     infectious disease, a neoplastic disease or as a thrombolytic agent. The
CC     antibodies can also be used for detection and diagnosis
XX
SQ     Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;

Query Match             100.0%;  Score 321; DB 2; Length 321;
Best Local Similarity   100.0%;  Pred. No. 1.1e-92;
  Matches 321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy       61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db       61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy      121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy      181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Qy      241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTCAACAGTTTCTCCATTCACGTTCGGTGCT 300
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Db      241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTCAACAGTTTCTCCATTCACGTTCGGTGCT 300

Qy      301 GGGACCAAGCTGGAGCTGAAA 321
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Db      301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 2
ADL35002
ID     ADL35002 standard; DNA; 321 BP.
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AC     ADL35002;
XX
DT     03-JUN-2004  (first entry)
XX
DE     Murine anti-tissue factor light chain antibody DNA SeqID 1.
XX
KW     murine; mouse; humanised antibody; variable domain; framework region; FR;
KW     huFR; immune system molecule; H36.D2.B7; ss; gene; anti-tissue factor.
XX
OS     Mus sp.
XX
FH     Key             Location/Qualifiers
FT     CDS             1..321
FT                     /tag= a
FT                     /partial
FT                     /product= "H36.D2.B7 light chain protein"
FT                     /note= "Start and stop codons are absent"
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PD     11-MAR-2004.
XX
PF     06-AUG-2003; 2003WO-US024637.
XX
PR     29-AUG-2002; 2002US-00230880.
XX
PA     (SUNO-) SUNOL MOLECULAR CORP.
XX
PI     Wong HC, Stinson JR, Mosquera LA;
XX
DR     WPI; 2004-239169/22.
DR     P-PSDB; ADL35003.
XX
PT     Producing humanized antibodies for diagnostic and therapeutic purposes
PT     comprises optimizing similarity between individual antibody framework
PT     regions to help identify human framework regions suitable for making the
PT     antibodies.
XX
PS     Disclosure; SEQ ID NO 1; 137pp; English.
XX
CC     This invention relates to a novel method for producing a humanised
CC     antibody variable (V) domain or its fragment by optimising sequence
CC     similarity between individual antibody framework regions (FRs) in order
CC     to identify suitable human FRs (huFRs). Specifically, it refers to novel
CC     immune system molecules i.e. humanised monoclonal antibodies that exhibit
CC     suitable binding affinity with reduced immunogenicity in humans. The
CC     present invention describes a method of mutagenising DNA of non-human FRs
CC     to encode humanised FRs having an amino acid sequence that is
CC     substantially identical to the selected human FR previously identified
CC     through sequence similarity searching. As such, this method provides
CC     humanised light or heavy chain V domains of the sequence huFR1-CDR1-huFR2
CC     -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic
CC     products to treat and/ or diagnose diseases in humans and animals.
CC     Furthermore, the method expands the number of best fit possibilities that
CC     can be generated and provides a rational basis for assembling nearly all
CC     humanised immune system molecules of interest. This polynucleotide
CC     sequence is a murine anti-tissue factor light chain antibody H36.D2.B7
CC     DNA of the invention.
XX
SQ     Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;

Query Match             100.0%;  Score 321; DB 12; Length 321;
Best Local Similarity   100.0%;  Pred. No. 1.1e-92;
  Matches 321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db        1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy       61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy      121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy      181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy      241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTCAACAGTTTCTCCATTCACGTTCGGTGCT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTCAACAGTTTCTCCATTCACGTTCGGTGCT 300

Qy      301 GGGACCAAGCTGGAGCTGAAA 321
            |||||||||||||||||||||
Db      301 GGGACCAAGCTGGAGCTGAAA 321
```

Wed Apr 19 10:36:15 2006

us-10-764-140-1.rng

Page 3

RESULT 3
ADU06807
ID   ADU06807 standard; DNA; 321 BP.
XX
AC   ADU06807;
XX
DT   10-FEB-2005 (first entry)
XX
DE   Murine H36.D2.B7 antibody VL encoding DNA SEQ ID NO:1.
XX
KW   ds; gene; septic shock syndrome; tissue factor; antibacterial;
KW   immunosuppressive; antibody; antibody therapy.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..321
FT   /*tag= a
FT   /product= "Antibody H36.D2.B7 light chain variable
FT   region"
FT   /partial
FT   /note= "No start/stop codon given"
FT   /transl_except= (pos:16. .21,aa:Ser)
FT   exon   16. .21
FT   /*tag= b
FT   misc_feature   70. .90
FT   /*tag= c
FT   /note= "Encodes hypervariable region CDR1"
FT   misc_feature   148. .168
FT   /*tag= d
FT   /note= "Encodes hypervariable region CDR2"
FT   misc_feature   265. .292
FT   /*tag= e
FT   /note= "Encodes hypervariable region CDR3"
XX
PN   US2004229282-A1.
XX
PD   18-NOV-2004.
XX
PF   22-JAN-2004; 2004US-00764140.
XX
PR   10-MAR-1997; 97US-00814806.
PR   16-APR-1999; 99US-00293854.
PR   12-NOV-2002; 2002US-00293417.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Wong HC, Jiao J;
XX
DR   WPI; 2004-813246/80.
DR   P-PSDB; ADU06808.
XX
PT   Treating or preventing septic shock syndrome in mammal, involves
PT   administering antibody that binds native human tissue factor and does not
PT   substantially bind non-native tissue factor.
XX
PS   Claim 43; SEQ ID NO 1; 28pp; English.
XX
CC   The invention relates to a novel method for treating or preventing (M1)
CC   septic shock syndrome in a mammal, involving administering to the mammal
CC   an effective amount of an antibody that binds native human tissue factor
CC   and does not substantially bind non-native tissue factor, where the
CC   factor X binding to the complex is inhibited and the administration is
CC   sufficient to prevent or treat the septic shock syndrome in the mammal.
CC   In (M1), the antibody has the binding specificity for native human tissue
CC   factor about equal to or greater than H36.D2.B7 (ATCC HB-12255), and is a
CC   monoclonal chimeric antibody. An antibody of the invention has
CC   antibacterial and immunosuppressive activity, and acts as an inhibitor of
CC   binding between factor X or factor VIa and tissue factor/factor VIIa
CC   complex. The present sequence encodes the light chain variable region of
CC   the murine antibody of the invention, H36.D2.B7.
XX
SQ   Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;

Query Match   100.0%; Score 321; DB 13; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.1e-92;
Matches 321; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCGCATCTCTGGGGAGAAAGTGTCACC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCGCATCTCTGGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy   241 GAAGATTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAAGATTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
             |||||||||||||||||||||
Db   301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 4
ADW07325
ID   ADW07325 standard; cDNA; 321 BP.
XX
AC   ADW07325;
XX
DT   07-APR-2005 (first entry)
XX
DE   Mouse anti-tissue factor antibody H36.D2.B7 VL cDNA.
XX
KW   Blood-clotting; light chain variable region; inflammation;
KW   antiinflammatory; antibody; BB; tissue factor; sepsis;
KW   disseminated intravascular coagulation; anticoagulant;
KW   hematological disease; thrombosis; lung injury; respiratory-gen.;
KW   respiratory distress syndrome; Immunosuppressive; Antibacterial;
KW   Antiarthritic; Antianemic; anemia; rheumatoid arthritis;
KW   glomerulonephritis; multiple sclerosis; psoriasis; sjogren's syndrome;
KW   inflammatory bowel disease.
XX
OS   Mus sp.
XX
FH   Key   Location/Qualifiers
FT   CDS   1. .321
FT   /*tag= a
FT   /product= "Light chain"
FT   /partial
FT   /note= "No start or stop codon shown"
XX
PN   WO2005004793-A2.
XX
PD   20-JAN-2005.
XX
PF   04-JUN-2004; 2004WO-US017900.
XX
PR   19-JUN-2003; 2003US-0480254P.
PR   22-JAN-2004; 2004US-0538892P.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Egan JO;
XX
DR   WPI; 2005-091964/10.
DR   P-PSDB; ADW07326.

XX
PT   antibody; tissue factor; blood-clotting; anticoagulant; vasotropic;
KW   thrombolytic; cardiovascular disease; infectious disease; neoplasm;
KW   thrombosis; restenosis; light chain variable region; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..321
FT   /tag= a
FT   /product= "H36.D2.B7 anti-tissue factor light chain
FT   variable region"
XX
PN   US2005089929-A1.
XX
PD   28-APR-2005.
XX
PF   11-JUL-2003; 2003US-00618338.
XX
PR   10-MAR-1997; 97US-00814806.
PR   16-APR-1999; 99US-00293854.
PR   12-NOV-2002; 2002US-00293417.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Wen J;
XX
DR   WPI; 2005-344279/35.
DR   P-PSDB; AD240937.
XX
PT   Antibodies binding to native human tissue factor without substantial
PT   binding to non-native tissue factor, useful for inhibiting blood
PT   coagulation, for reducing tissue factor levels in a mammal, and for
PT   detecting tissue factor.
XX
PS   Claim 11; SEQ ID NO 1; 36pp; English.
XX
CC   The invention relates to an antibody (I) that binds native human tissue
CC   factor and does not substantially bind non-native tissue factor. Also
CC   described: (1) an isolated nucleic acid (II) comprising a sequence
CC   encoding at least a portion of an antibody that binds native human tissue
CC   factor; (2) a recombinant vector (IV) comprising (II), where (IV) can
CC   express at least a portion of an antibody that binds native human tissue
CC   factor; (3) a host cell (V) comprising (IV); (4) inhibiting (M1) blood
CC   coagulation in a mammal by administering the antibody, where the antibody
CC   complexes with native tissue factor and factor X binding to the complex
CC   is inhibited; (5) reducing (M2) tissue factor levels in a mammal by
CC   administering the antibody covalently linked to a cell toxin or to an
CC   effector molecule to provide complement-fixing ability and antibody-
CC   dependent cell-mediated cytotoxicity, where the antibody contacts cells
CC   expressing tissue factor to reduce tissue factor levels in the mammal;
CC   and (6) detecting (M3) tissue factor in a biological sample comprising
CC   contacting the sample with the antibody (I), where the antibody is
CC   monoclonal. (I) is useful for inhibiting blood coagulation in a mammal
CC   (preferably human), for reducing tissue factor levels in a mammal, and
CC   for detecting tissue factor in a biological sample. (I) can be used in
CC   the treatment of a thromboembolic condition associated with
CC   cardiovascular disease, an infectious disease, or a neoplastic disease,
CC   such as thrombosis and restenosis. The antibodies of the invention
CC   (especially H36.D2.B7 (secreted by hybridoma ATCC HB-12255)) bind
CC   strongly to a conformational epitope in native human tissue factor and do
CC   not substantially bind to non-native or denatured tissue factor. The
CC   antibodies prevent conversion of factor X to its activated form factor
CC   Xa. The present sequence encodes the H36.D2.B7 anti-tissue factor light
CC   chain variable region.
XX
SQ   Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;

Query Match   100.0%; Score 321; DB 14; Length 321;
Best Local Similarity   100.0%; Pred. No. 1.1e-92;
Matches 321; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

XX
PT   Preventing or treating sepsis or inflammation in mammals comprises
PT   administering a humanized or chimeric antibody that binds to a human
PT   tissue factor to form a complex in which factor X or IX binding to the
PT   complex is inhibited.
XX
PS   Disclosure; SEQ ID NO 1; 109pp; English.
XX
CC   The invention relates to preventing or treating a sepsis or inflammatory
CC   disease in a mammal comprising administering to the mammal a therapeutic
CC   amount of at least one humanized antibody, chimeric antibody, or their
CC   fragment that binds specifically to tissue factor (TF) to form a complex,
CC   where factor X or IX binding to the complex is inhibited and the
CC   administration prevents or treats the sepsis in the mammal. Also included
CC   are a kit for performing the above method and reducing an inflammatory
CC   cycokine production in a mammal. The inflammatory disease is associated
CC   with arthritis (preferably rheumatoid arthritis), glomerulonephritis,
CC   multiple sclerosis, psoriasis, Sjogren's syndrome, or inflammatory bowel
CC   disease. The method also treats or prevents a sepsis-induced anemia or a
CC   sepsis-related condition in a mammal, where the sepsis-related condition
CC   is DIC, fibrin deposition, thrombosis, lung injury, or sepsis-associated
CC   renal disorder. The lung injury is acute lung injury (ALI) or acute
CC   respiratory distress syndrome (ARDS). The sepsis-associated renal
CC   disorder is acute tubular necrosis. The methods and kit are useful for
CC   preventing or treating sepsis or sepsis-related conditions (e.g. DIC or
CC   anemia) or inflammatory diseases (e.g. arthritis). The humanized
CC   antibodies are based on the chimeric antibody cH36 which comprises the
CC   light and heavy chain variable regions (VL or VH) of an anti-TF antibody
CC   fused to the human IgG4 heavy and kappa light constant regions. The CDRs
CC   (complementarity determining region) and FRs (framework regions) are then
CC   humanized. The present sequence encodes the light or heavy chain variable
CC   region of the anti-TF antibody (wild-type).
XX
SQ   Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;

Query Match   100.0%; Score 321; DB 14; Length 321;
Best Local Similarity   100.0%; Pred. No. 1.1e-92;
Matches 321; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy 181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTTCTCCATTCACGTTCGGTGCT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTTCTCCATTCACGTTCGGTGCT 300

Qy 301 GGGACCAAGCTGGAGCTGAAA 321
        |||||||||||||||||||||
Db 301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 5
AD240936
ID   AD240936 standard; DNA; 321 BP.
XX
AC   AD240936;
XX
DT   14-JUL-2005 (first entry)
XX
DE   H36.D2.B7 anti-tissue factor light chain variable region encoding DNA.

```
Qy    1  GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC    60

Qy   61  ATCACATGCCTGGCAAGTCAGCAGCCATTGATAGTATGGTTAGCAGCAGAAACCA        120
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  ATCACATGCCTGGCAAGTCAGCAGCCATTGATAGTATGGTTAGCAGCAGAAACCA        120

Qy  121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATCAGCGAGTGGGTCCCATCA  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATCAGCGAGTGGGTCCCATCA  180

Qy  181  AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT      240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT      240

Qy  241  GAAGATTTTGTAAATTATTTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT   300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  GAAGATTTTGTAAATTATTTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT   300

Qy  301  GGGACCAAGCTGGAGCTGAAA    321
         |||||||||||||||||||||
Db  301  GGGACCAAGCTGGAGCTGAAA    321
```

RESULT 6
ACC58568
ID   ACC58568 standard; cDNA; 322 BP.
XX
AC   ACC58568;
XX
DT   26-AUG-2003 (first entry)
XX
DE   Anti-tissue factor antibody H36.D2.B7 VL coding sequence.
XX
KW   Tissue factor; antibody; H36.D2.B7; anticoagulant; cytostatic;
KW   antiinflammatory; mouse; gene; ss.
OS   Mus sp.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..322
FT   /tag= a
FT   /partial
FT   /product= "H36.D2.B7 VL"
FT   /transl_except= (pos:256..259,aa:Tyr)
FT   /note= "this codon has an apparent 1 nucleotide insertion
FT   which alters the reading frame; the CDS has no start or
FT   stop codon"
XX
PN   WO2003037911-A2.
XX
PD   08-MAY-2003.
XX
PF   29-OCT-2002; 2002WO-US034727.
XX
PR   29-OCT-2001; 2001US-0343306P.
PR   21-NOV-2001; 2001US-00990586.
XX
PA   (SUNO-) SUNOL MOLECULAR CORP.
XX
PI   Jiao J, Wong HC, Nieves EL, Mosquera LA;
XX
DR   WPI; 2003-468399/44.
DR   P-PSDB; ABR42699.
XX
PT   New humanized antibody that binds specifically to human tissue factor,
PT   useful for in vivo diagnostic methods, or for inhibiting blood
PT   coagulation or blood clot formation, angiogenesis, tumor metastases or
PT   inflammation in a mammal.
XX
PS   Example 1; Fig 1A; 110pp; English.
XX

CC   The present sequence is the coding sequence for the light chain variable
CC   region (VL) of anti-recombinant human tissue factor (TF) murine antibody
CC   H36.D2.B7 (ATCC HB-12255). The invention relates to antibodies,
CC   especially humanized H36.D2.B7, that provide superior anticoagulant
CC   activity by binding native human TF with high affinity and specificity.
CC   The antibodies bind human TF, either alone or present in a TF:Factor VIIa
CC   complex, effectively preventing Factor X (or Factor IX) binding to TF or
CC   the complex, and thereby reducing blood coagulation. The humanized
CC   antibodies are useful for inhibiting blood coagulation or blood clot
CC   formation, angiogenesis, tumour metastases or inflammation in a mammal.
CC   They are also useful as drug carriers, as cytotoxic agents, for reducing
CC   TF levels in mammals, and for in vivo diagnosis
XX
SQ   Sequence 322 BP; 85 A; 80 C; 73 G; 84 T; 0 U; 0 Other;

Query Match   96.6%; Score 310; DB 9; Length 322;
Best Local Similarity   99.7%; Pred. No. 3.8e-89;
Matches 321; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

```
Qy    1  GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC    60

Qy   61  ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTTAGCAGCAGAAACCA  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTTAGCAGCAGAAACCA  120

Qy  121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTCTTCAAGATCAGCGAGTGGGTCCCATCA  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTCTTCAAGATCAGCGAGTGGGTCCCATCA  180

Qy  181  AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT      240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT      240

Qy  241  GAAGATTTTGTAAATTA-TTACTGTCAACAAGTTTACAGTTTACAGTTCCATTCACGTTCGGTGC    299
         ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db  241  GAAGATTTTGTAAATTATTTACTGTCAACAAGTTTACAGTTTACAGTTCCATTCACGTTCGGTGC    300

Qy  300  TGGGACCAAGCTGGAGCTGAAA    321
         ||||||||||||||||||||||
Db  301  TGGGACCAAGCTGGAGCTGAAA    322
```

RESULT 7
AAZ33012
ID   AAZ33012 standard; DNA; 375 BP.
XX
AC   AAZ33012;
XX
DT   26-JAN-2000 (first entry)
XX
DE   Anti-tissue factor mouse monoclonal antibody ATR-2 L chain V region DNA.
XX
KW   Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW   ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW   disseminated intravascular coagulation; immunogenicity; chimeric; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
PN   WO9951743-A1.
XX
PD   14-OCT-1999.
XX
PF   02-APR-1999; 99WO-JP001768.
XX
PR   03-APR-1998; 98JP-00091850.
XX
PA   (CHUS) CHUGAI SEIYAKU KK.
XX
PI   Sato K, Adachi H, Yabuta N;
XX

Left column

```
DR   WPI; 1999-620204/53.
DR   P-PSDB; AAY52761.
XX
PT   Humanised antibody recognizing human tissue factor, used for treatment of
PT   disseminated intravascular coagulation.
XX
PS   Example 1; Page 190-191; 291pp; Japanese.
XX
CC   The present invention describes chimeric antibody (Ab) heavy (H) chains
CC   containing the variable region of the H chain of a mouse monoclonal Ab
CC   recognising human tissue factor (hTF) and the constant region of the H
CC   chain of a human Ab. The variable region is one of six specified
CC   sequences (which are the H chain variable regions from mouse monoclonal
CC   Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC   containing the variable region of the L chain of a mouse monoclonal Ab
CC   recognising human tissue factor (hTF) and the constant region of the L
CC   chain of a human Ab, the variable region being one of six specified
CC   sequences (which are the L chain variable regions from mouse monoclonal
CC   Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC   and prevention of thrombotic disease, especially of disseminated
CC   intravascular coagulation (DIC). The humanised antibody has the high hTF
CC   binding activity of the mouse monoclonal antibody but greatly reduced
CC   immunogenicity. AAZ33001 to AAZ33091 and Y52007 to AAY52767 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 375 BP; 96 A; 89 C; 92 G; 98 T; 0 U; 0 Other;

Query Match        91.5%;   Score 293.8;  DB 2;  Length 375;
Best Local Similarity   94.7%;  Pred. No. 6.5e-84;
Matches  304;  Conservative   0;  Mismatches  17;  Indels   0;  Gaps   0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC  60
            |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     55 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 114

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 174

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            ||||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||||
Db    175 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCAACCAGCTTGGCAGATGGGGTCCCATCA 234

Qy    181 AGGTTCAGTGGCAGTGGATCTGGGACAGACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
            |||||||||||| |||||| ||||  ||||||||||||||||||||||||||||||||||||
Db    235 AGGTTCAGTGGTGGTAGTGGGATCGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 294

Qy    241 GAAGATTTTGTGAAATTATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
            |||||||||||| ||| ||| |||||||||||||| |||||||| ||||||||||||||
Db    295 GAAGATTTTGTGAAGTTATTACTGTCAACAACTTTACAGTACTCCGTACACGTTCGGAGGG 354

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
            ||||||||||||| | |||
Db    355 GGGACCAAGCTGGAAATAAAA 375

RESULT 8
AAZ33013
ID   AAZ33013 standard; DNA; 375 BP.
XX
AC   AAZ33013;
XX
DT   26-JAN-2000  (first entry)
XX
DE   Anti-tissue factor mouse monoclonal antibody ATR-3 L chain V region DNA.
XX
KW   Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW   ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW   disseminated intravascular coagulation; immunogenicity; chimeric; ss.
XX
OS   Synthetic.
OS   Mus sp.
XX
```

Right column

```
PN   WO951743-A1.
XX
PD   14-OCT-1999.
XX
PF   02-APR-1999;  99WO-JP001768.
XX
PR   03-APR-1998;  98JP-00091850.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Sato K,  Adachi H,  Yabuta N;
XX
DR   WPI; 1999-620204/53.
DR   P-PSDB; AAY52762.
XX
PT   Humanised antibody recognizing human tissue factor, used for treatment of
PT   disseminated intravascular coagulation.
XX
PS   Example 1; Page 192; 291pp; Japanese.
XX
CC   The present invention describes chimeric antibody (Ab) heavy (H) chains
CC   containing the variable region of the H chain of a mouse monoclonal Ab
CC   recognising human tissue factor (hTF) and the constant region of the H
CC   chain of a human Ab. The variable region is one of six specified
CC   sequences (which are the H chain variable regions from mouse monoclonal
CC   Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC   containing the variable region of the L chain of a mouse monoclonal Ab
CC   recognising human tissue factor (hTF) and the constant region of the L
CC   chain of a human Ab, the variable region being one of six specified
CC   sequences (which are the L chain variable regions from mouse monoclonal
CC   Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC   and prevention of thrombotic disease, especially of disseminated
CC   intravascular coagulation (DIC). The humanised antibody has the high hTF
CC   binding activity of the mouse monoclonal antibody but greatly reduced
CC   immunogenicity. AAZ33001 to AAZ33091 and Y27007 to AAY52767 represent
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 375 BP; 96 A; 88 C; 93 G; 98 T; 0 U; 0 Other;

Query Match        91.0%;   Score 292.2;  DB 2;  Length 375;
Best Local Similarity   94.4%;  Pred. No. 2.1e-83;
Matches  303;  Conservative   0;  Mismatches  18;  Indels   0;  Gaps   0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC  60
            |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     55 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 114

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 174

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            ||||||||||||||||||||| |||||||||  ||||||||||||||||||||||||||
Db    175 GGGAAATCTCCTCAGCTCCTGATTTATGCGCAACCAGCTTGGCAGATGGGGTCCCATCA 234

Qy    181 AGGTTCAGTGGCAGTGGATCGGACAGACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
            |||||||||||| |||||| |||  |||||||||||||||||||||||||||||||||||
Db    235 AGGTTCAGTGGTGTAGTGGGATCGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 294

Qy    241 GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
            ||||||||||| ||| ||| |||||||||||||| |||||||| ||||||||||||||
Db    295 GAAGATTTTGTGAAGTTATTACTGTCAACAACTTTACAGTACTCCGTACACGTTCGGAGGG 354

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
            ||||||||||||| | |||
Db    355 GGGACCAAGCTGGAAATAAAA 375

RESULT 9
AD251613
ID   AD251613 standard; DNA; 949 BP.
XX
AC   AD251613;
```

```
XX
DT   30-JUN-2005  (first entry)
XX
DE   High-functioning protein related DNA SEQ ID NO 114.
XX
KW   cytostatic; hypotensive; nucleic acid library; cancer; neoplasm;
KW   hypertension; cardiovascular disease; ds; gene.
XX
OS   Unidentified.
XX
PN   WO200503575l-Al.
XX
PD   21-APR-2005.
XX
PF   15-OCT-2004; 2004WO-JP015290.
XX
PR   15-OCT-2003; 2003JP-00355702.
XX
PA   (UYKE-) UNIV KEIO.
XX
PI   Yanagawa H,  Tabata N,  Kojoh K;
XX
DR   WPI; 2005-346216/35.
DR   P-PSDB; ADZ51614.
XX
PT   Selecting a high-functioning protein which is useful for treating cancer
PT   and hypertension, comprises selecting a protein interacting with a target
PT   molecule.
XX
PS   Disclosure; SEQ ID NO 114; 92pp; Japanese.
XX
CC   The invention relates to a method of selecting a high-functioning protein
CC   which comprises constructing a protein-coding DNA library, transcribing
CC   DNAs, attaching a spacer to the 3' end of transcribed RNAs and
CC   constructing a library of molecules assigned to genotype and phenotype in
CC   a cell-free translation system, treating the library of assigned
CC   molecules, binding an assigned molecule to a target molecule and
CC   amplifying nucleic acid. The method is useful for selecting a high-
CC   functioning protein by selecting a protein interacting with a target
CC   molecule. The method is useful for manufacturing a protein which
CC   interacts with a target molecule. The single stranded antibodies are
CC   useful for treating cancer and hypertension. The method is rapid and
CC   efficient. The present sequence represents a high-functioning protein
CC   related DNA.
XX
SQ   Sequence 949 BP; 248 A; 220 C; 259 G; 222 T; 0 U; 0 Other;

Query Match             90.0%;  Score 289;  DB 14;  Length 949;
Best Local Similarity   93.8%;  Pred. No. 3.3e-82;
Matches  301;  Conservative   0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 GACATTCAGATGACCAGTCTCCTGCCTCCCAGTCGCATCTCTGGGAGAAAGTGTCACC 60
              ||||||||||||| ||||||||||||| ||||||||||||||||||||||||||||||||
Db        552 GACATTCAGATGACACAGTCTTCCTGCCTCCCCAGTCGCATCTCTGGGAGAAAGTGTCATC 611

Qy         61 ATCACATGCCTGGCAAGTCAGACCATTGATGACATGGTTAGCATGGTTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 ATCACATGCCTGGCAAGTCAGACCATTGGTACATTGGTTAGCATGGTTATCAGCAGAAACCA 671

Qy        121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        672 GGGAAATCTCCTCTTCAGCTCCTGATTTATGCTGCCAACCAGCTGGGCAGATGGGGTCCCATCA 731

Qy        181 AGGTTCAGTGGCAGTGGATCTGGGACACAAAATTTCTCTTCAAGATCAGCAGCCTACAGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 AGGTTCAGTGGCAGTGGATCTGGGACACAAAATTTCTTCTTCAAGATCAGCAGCCTACAGGCT 791

Qy        241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
              ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        792 GAAGATTTTGTAAGTTATTATTACTGTCAACAACTTTACAGTACTCCGTGGACGTTCGGTGGA 851

Qy        301 GGGACCAAGCTGGAGCTGAAA 321
              || ||||||||||||||||| |||
```

Db   852 GGTACCAAGCTGGAAATCAAA 872

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                                      RESULT 10
Db   AAF76338
     ID   AAF76338 standard; DNA; 1135 BP.
     XX
     AC   AAF76338;
     XX
     DT   05-JUN-2001  (first entry)
     XX
     DE   Anti-VHSV single chain antibody BU1-encoding DNA.
     XX
     KW   Anti-VHSV; single chain antibody BU1; ScAb; scFv;
     KW   monoclonal antibody 3F1H10; variable region; antiviral; anti-allergy;
     KW   human kappa light chain constant domain; vaccine; gene therapy;
     KW   rainbow trout TGF-beta signal peptide; transforming growth factor beta;
     KW   genetic prophylaxis; ds.
     XX
     OS   Oncorhynchus mykiss.
     OS   Mus musculus.
     OS   Homo sapiens.
     OS   Synthetic.
     OS   Chimeric.
     XX
     FH   Key         Location/Qualifiers
     FT   misc_feature  1..9
     FT               /*tag=   a
     FT               /note= "Derived from Invitrogen pCDNA3"
     FT   CDS         13..1122
     FT               /*tag=   c
     FT               /product= "Single chain antibody BU1"
     FT   misc_feature  1126..1135
     FT               /*tag=   b
     FT               /note= "BU1 insert region"
     FT   misc_feature  1126..1135
     FT               /*tag=   d
     FT               /note= "Derived from Invitrogen pCDNA3"
     XX
     PN   WO200121800-A1.
     XX
     PD   29-MAR-2001.
     XX
     PF   20-SEP-2000; 2000WO-GB003605.
     XX
     PR   20-SEP-1999;  99DK-00001329.
     XX
     PA   (UYAB-) UNIV ABERDEEN.
     PA   (STAT-) STATENS VETERINAERE SERUMLABORATOTIUM.
     XX
     PI   Secombes CJ,  Cunningham C,  Lorenzen N;
     XX
     DR   WPI; 2001-257991/26.
     DR   P-PSDB; AAB73388.
     XX
     PT   New non-infectious nucleic acid construct encoding recombinant antibody
     PT   molecule, useful for conferring protective immunity to infectious
     PT   diseases, preventing allergic reactions or reactions caused by toxins in
     PT   animals.
     XX
     PS   Example; Page 9-10; 29pp; English.
     XX
     CC   The invention relates to a non-infectious nucleic acid construct encoding
     CC   a recombinant (e.g., single chain) antibody molecule. The nucleic acid
     CC   construct is adapted for in vivo establishment of protective immunity to
     CC   an infectious disease in an animal, or is formulated for in vivo
     CC   prevention of an allergic reaction to an allergen or a reaction caused by
     CC   the presence of a toxic substance in an animal. Constructs of the
     CC   invention are thus useful for treating infectious disease caused by viral
     CC   haemorrhagic septicaemia virus (VHSV) (fish), infectious haemotopoietic
     CC   necrosis virus (fish), bovine viral diarrhoea virus, pseudorabies virus
     CC   (pigs), plasmocytosis virus (mink), feline leukaemia virus, human
     CC   immunodeficiency virus, and hepatitis A virus (human). Genetic
```

```
FT   CDS                          /product= "variable heavy chain region"
FT                                523. .1290
FT                                /*tag= b
FT                                /product= "variable light chain-Fc fusion protein"
FT   misc_feature                 601. .902
FT                                /*tag= d
FT                                /product= "variable light chain"
FT   misc_feature                 928. .1101
FT                                /*tag= e
FT                                /note= "Fc binding domain-like structure"
FT   misc_feature                 1102. .1275
FT                                /*tag= f
FT                                /note= "Fc binding domain-like structure"
XX
PN   EP675199-A2.
XX
DR   04-OCT-1995.
XX
PF   14-MAR-1995;  95EP-00301664.
XX
PR   30-MAR-1994;  94JP-00082693.
XX
PA   (TAKI ) TAKARA SHUZO CO LTD.
XX
PI   Yoshinobu O, Atsushi O, Hirofumi Y, Takashi T, Ikunoshin K;
XX
DR   WPI; 1995-338286/44.
DR   P-PSDB; AAR92828, AAR92829.
XX
PT   Gene encoding variable region of anti-human influenza A type virus
PT   antibody - useful for prodn. of artificial antibodies.
XX
PS   Example 4; Page 32-35; 42pp; English.
XX
CC   This sequence encodes the C179Fv-PP fusion polypeptide. The encoded
CC   sequence is an anti-human influenza A type virus antibody. The antibody
CC   recognises the stem region of the haemagglutinin (HA) molecule of the
CC   H1N1 and H2N2 subtypes of human influenza A type virus, and shows
CC   neutralisation activity against these two subtypes. The antibody shows no
CC   recognition of the H3N2 subtype. Artificial antibodies (such as this) and
CC   polypeptides are useful in the diagnosis and treatment of human
CC   influenza. As the antibodies recognise the stem region of the HA
CC   molecule, the influenza virus will be recognised even if the HA
CC   changes. This provides an advantage over current vaccines, as the virus
CC   periodically alters it's HA molecule
XX
SQ   Sequence 1300 BP;  393 A;  319 C;  289 G;  299 T;  0 U;  0 Other;
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Query Match             89.4%;  Score 287;  DB 2;  Length 1300;
Best Local Similarity   93.7%;  Pred. No. 1.7e-81;
Matches 299;  Conservative   0;  Mismatches  20;  Indels   0;  Gaps    0;

Qy        1 GACATTCAGATGACCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
            |||||  || ||||||||||||||||||||||||||||||||||||||||||||||||
Db      589 GACATCGAGCTCACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 648

Qy       61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGCATGGTATCAGCAGAAACCA 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      649 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGCATGGTATCAGCAGAAACCA 708

Qy      121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db      709 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCAACCAGTTGGCAGATGGGGTCCCATCA 768

Qy      181 AGGTTCAGTGGCAGTGGATCTGGGACAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db      769 AGGTTCAGTGGCAGTGGATCTGGCACCAGTTTCTTTCAAGATCAGCAGCCTACAGGCT 828

Qy      241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
            ||||||||||||| |||| |||||||||||||||||||||| |||||||||||||||||
Db      829 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTTCACGTTCGGTGGA 888

Qy      301 GGGACCAAGCTGGAGCTGA 319
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Db   889 GGCACCAAGCTGGAGTCGA 907
         |||||||||||||||| ||
```

RESULT 12
ADZ51605
ID   ADZ51605 standard; DNA; 949 BP.
XX
AC   ADZ51605;
XX
DT   30-JUN-2005 (first entry)
XX
DE   High-functioning protein related DNA SEQ ID NO 106.
XX
KW   cytostatic; hypotensive; nucleic acid library; cancer; neoplasm;
KW   hypertension; cardiovascular disease; ds; gene.
XX
OS   Unidentified.
XX
PN   WO2005035751-A1.
XX
PD   21-APR-2005.
XX
PF   15-OCT-2004; 2004WO-JP015290.
XX
PR   15-OCT-2003; 2003JP-00355702.
XX
PA   (UYKB-) UNIV KEIO.
XX
PI   Yanagawa H, Tabata N, Kojoh K;
XX
DR   WPI; 2005-346216/35.
DR   P-PSDB; ADZ51606.
XX
PT   Selecting a high-functioning protein which is useful for treating cancer
PT   and hypertension, comprises selecting a protein interacting with a target
PT   molecule.
XX
PS   Disclosure; SEQ ID NO 106; 92pp; Japanese.
XX
CC   The invention relates to a method of selecting a high-functioning protein
CC   which comprises constructing a protein-coding DNA library, transcribing
CC   DNAs, attaching a spacer to the 3' end of transcribed RNAs and
CC   constructing a library of molecules assigned to genotype and phenotype in
CC   a cell-free translation system, treating the library of assigned
CC   molecules, binding an assigned molecule to a target molecule and
CC   amplifying nucleic acid. The method is useful for selecting a high-
CC   functioning protein by selecting a protein interacting with a target
CC   molecule. The method is useful for manufacturing a protein which
CC   interacts with a target molecule. The single stranded antibodies are
CC   useful for treating cancer and hypertension. The method is rapid and
CC   efficient. The present sequence represents a high-functioning protein
CC   related DNA.
XX
SQ   Sequence 949 BP; 247 A; 221 C; 261 G; 220 T; 0 U; 0 Other;

Query Match   89.0%; Score 285.8; DB 14; Length 949;
Best Local Similarity   93.1%; Pred. No. 3.6e-81;
Matches 299; Conservative   0; Mismatches   22; Indels   0; Gaps   0;

```
Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
        ||||||||||||| ||||||||||||||||||||| |||||||| ||||||||||||||
Db  552 GACATTCAGATGACGACAGTTTCCTGCCTCCCAGTTTGCATCTTTGGGAGAAAGTGTCATC 611

Qy   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAAACCA 120
        ||||||||||||||||||||||  |||||||| |||||||||||||||||||||||||||
Db  612 ATCACATGCTGGCAAGTCAGACCATTGGTACATGGTTAGCATGTATCAGCAGAAAACCA 671

Qy  121 GGGAAATCCCTGATTATGCTGCCACCAACTTGGCAGATGGGTCCATCA 180
        |||||||||||||||||||||||  ||||||||||||||||||||||||
Db  672 GGGAAATCCCTGATTATGCTGCCACCAGCTGGGCAGATGGGTCCATCA 731

Qy  181 AGGTTCAGTGCAGTGGGATCTGGACACAAAATTTTCTTTCCAAGATCAGCAGCCTACAGGCT 240
```

```
Db  732 AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTTCTTTCCAAGATCAGCAGCCTACAGGCT 791
        ||||||||| |||||||||||| |||||||||||||||||||||||||||||||||||||

Qy  241 GAAGATTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
        ||||||||||| ||||| |||||||||||||||| |||| || |||||||||||||
Db  792 GAAGATTTGTAAGTTATTATTACTGTCAACAACTTACAGTAGTCCGTGACGTTCGGTGGA 851

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
        || |||||||||||| |||| |
Db  852 GGCACCAAGCTGGAAATCAAA 872
```

RESULT 13
AAT04180
ID   AAT04180 standard; cDNA to mRNA; 1228 BP.
AC   AAT04180;
XX
DT   09-MAY-1996 (first entry)
XX
DE   scFv-PP coding sequence.
XX
KW   Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;
KW   haemagglutinin; variable heavy chain; therapy; ds.
XX
OS   Synthetic.
XX
FH   Key   Location/Qualifiers
FT   CDS   40..1218
FT   /*tag= a
FT   /product= "scFv-PP"
FT   misc_feature   106..471
FT   /*tag= b
FT   /product= "variable heavy chain"
FT   misc_feature   529..830
FT   /*tag= c
FT   /product= "variable light chain"
FT   misc_feature   856..1029
FT   /*tag= d
FT   /note= "Fc binding domain-like structure"
FT   misc_feature   1030..1203
FT   /*tag= e
FT   /note= "Fc binding domain-like structure"
XX
PN   EP675199-A2.
XX
PD   04-OCT-1995.
XX
PF   14-MAR-1995; 95EP-0301664.
XX
PR   30-MAR-1994; 94JP-00082693.
XX
PA   (TAKI) TAKARA SHUZO CO LTD.
XX
PI   Yoshinobu O, Atsushi O, Hirofumi Y, Takashi T, Ikunoshin K;
XX
DR   WPI; 1995-338286/44.
DR   P-PSDB; AAR82835.
XX
PT   Gene encoding variable region of anti-human influenza A type virus
PT   antibody - useful for prodn. of artificial antibodies.
XX
PS   Example 4; Page 36-38; 42pp; English.
XX
CC   This sequence encodes the scFv-PP fusion polypeptide. The encoded
CC   sequence is an anti-human influenza A type virus antibody. The antibody
CC   recognises the stem region of the haemagglutinin (HA) molecule of the
CC   H1N1 and H2N2 subtypes of human influenza A type virus, and shows
CC   neutralisation activity against these two subtypes. The antibody shows no
CC   recognition of the H3N2 subtype. Artificial antibodies (such as this) and
CC   polypeptides are useful in the diagnosis and treatment of human
CC   influenza. As the antibodies recognise the stem region of the HA
CC   molecule, the influenza virus will be recognised even if the HA molecule

```
CC   changes. This provides an advantage over current vaccines, as the virus
CC   periodically alters it's HA molecule
XX
SQ   Sequence 1228 BP; 362 A; 305 C; 282 G; 279 T; 0 U; 0 Other;

Query Match     88.9%;  Score 285.4; DB 2; Length 1228;
Best Local Similarity  93.4%;  Pred. No. 5.3e-81;
Matches  298;  Conservative  0;  Mismatches  21;  Indels  0;  Gaps  0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
          |||||| ||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 GACATCGAGCTCACCCAGTCTCCTGCCTCCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 576

Qy     61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 ATCACATGCTGGCGAGTCTGCGGCACCATTGGTACATGGTTAGCATGGTATCAGCAGAAACCA 636

Qy    121 GGGAAATCTTCCTCAGCTCCTGATTTATGTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    637 GGGAAATCTTCCTCAGCTCCTGATTTATGTGCCAACCAGCTTGGCAGATGGGGTCCCATCA 696

Qy    181 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTTCTTTCCCTTCAAGATCAGCAGCCTACAGGCT 240
          ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    697 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTTCCCTTCAAGATCAGCAGCCTACAGGCT 756

Qy    241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
          |||||||||||||| ||||||||||||||||||||||||| ||||||| |||||||||||
Db    757 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTGACGGTTCGGTGGA 816

Qy    301 GGGACCAAGCTGGAGCTGA 319
          ||||||||||||||||||||
Db    817 GGCACCAAGCTGGAGCTGA 835
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```
RESULT 14
AAK99183
ID   AAK99183 standard; DNA; 324 BP.
XX
AC   AAK99183;
XX
DT   12-JUN-2002  (first entry)
XX
DE   324nt DNA sequence of the invention.
XX
KW   Mouse monoclonal antibody; murine; surface antigen presl epitope;
KW   hepatitis B virus; gene; ds.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..324
FT                   /tag= a
FT                   /product= "Protein of the invention"
XX
PN   KR99008647-A.
XX
PD   05-FEB-1999.
XX
PF   02-JUL-1997;  97KR-00030694.
XX
PR   02-JUL-1997;  97KR-00030694.
XX
PA   (KORE-) KOREA RES INST CHEM TECHNOLOGY.
XX
PI   Hong HJ, Ryoo CJ;
XX
DR   WPI; 2000-168375/15.
DR   P-PSDB; AAO20094.
XX
PT   Changeable region of mouse monoclonal antibody recognizing surface
PT   antigen presl epitope of hepatitis B virus and gene.
XX
PS   Disclosure; Page 9; 14pp; Korean.
```

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XX
CC   The invention relates to a changeable region of mouse monoclonal antibody
CC   recognising surface antigen presl epitope of hepatitis B virus and gene.
CC   This polynucleotide sequence relates to a 324nt DNA of the invention
XX
SQ   Sequence 324 BP; 86 A; 77 C; 78 G; 83 T; 0 U; 0 Other;

Query Match     88.5%;  Score 284.2; DB 3; Length 324;
Best Local Similarity  92.8%;  Pred. No. 7.5e-81;
Matches  299;  Conservative  0;  Mismatches  23;  Indels  0;  Gaps  0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
          |||||| ||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GATATCGTGCTCACTCAGTCTCCTGCCTCCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy     61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATCACATGCTGGCGAGTCTGCGAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy    121 GGGAAATCTTCCTCAGCTCCTGATTTATGTGCCAGATGGGGTCCCATCA 180
          |||||||||||||||||||||||||||||||| ||||||||||||||||
Db    121 GGGAAATCTTCCTCAGCTCCTGATTTATGTGCCAACCAGCTTGGCAACCAGCTTGGGGTCCCATCA 180

Qy    181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGGTTCAGTGGCAGTGGTAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy    241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTCTCCATTCACGTTCGGTGCT 300
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    241 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTACACGTTCGGAGGG 300

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
          ||| |||||||||||
Db    301 GGGACCAAGCTTGGGAAATAAAA 321
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RESULT 15
AD251609
ID   AD251609 standard; DNA; 949 BP.
XX
AC   AD251609;
XX
DT   30-JUN-2005  (first entry)
XX
DE   High-functioning protein related DNA SEQ ID NO 110.
XX
KW   cytostatic; hypotensive; nucleic acid library; cancer; neoplasm;
KW   hypertension; cardiovascular disease; ds; gene.
XX
OS   Unidentified.
XX
PN   WO200503751-A1.
XX
PD   21-APR-2005.
XX
PF   15-OCT-2004; 2004WO-JP015290.
XX
PR   15-OCT-2003; 2003JP-00355702.
XX
PA   (UYKE-) UNIV KEIO.
XX
PI   Yanagawa H, Tabata N, Kojoh K;
XX
DR   WPI; 2005-346216/35.
DR   P-PSDB; AD251610.
XX
PT   Selecting a high-functioning protein which is useful for treating cancer
PT   and hypertension, comprises selecting a protein interacting with a target
PT   molecule.
XX
PS   Disclosure; SEQ ID NO 110; 92pp; Japanese.
XX
CC   The invention relates to a method of selecting a high-functioning protein
```

CC   which comprises constructing a protein-coding DNA library, transcribing
CC   DNAs, attaching a spacer to the 3' end of transcribed RNAs and
CC   constructing a library of molecules assigned to genotype and phenotype in
CC   a cell-free translation system, treating the library of assigned
CC   molecules, binding an assigned molecule to a target molecule and
CC   amplifying nucleic acid. The method is useful for selecting a high-
CC   functioning protein by selecting a protein interacting with a target
CC   molecule. The method is useful for manufacturing a protein which
CC   interacts with a target molecule. The single stranded antibodies are
CC   useful for treating cancer and hypertension. The method is rapid and
CC   efficient. The present sequence represents a high-functioning protein
CC   related DNA.
XX
SQ   Sequence 949 BP; 248 A; 218 C; 259 G; 224 T; 0 U; 0 Other;

Query Match   88.0%; Score 282.6; DB 14; Length 949;
Best Local Similarity   92.5%; Pred. No. 3.8e-80;
Matches 297; Conservative   0; Mismatches   24; Indels   0; Gaps   0;

Qy   1 GACAATTCAGATGACCCAGTCTCCTGCCTCCCAGTCGCATCTCTGGGAGAAAGTGTCACC   60
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Db   552 GACAATTCAGATGACACAGTTTCCTGCCTCCCAGTCGCATTTCTGGGAGAAAGTGTCATC 611

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||||| ||||||||||||||||| |||||||||||
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Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCGAGATGGGTCCCATCA 180
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Db   672 GGGAAATTTCCTCAGCTCCTGATTTATGCTGCAACCAGCTGGGCAGATGGGTCCCATCA 731

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Db   732 AGGTTCAGTGGTAGTGGATTTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 791

Qy   241 GAAGATTTTGTAAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGTGCT 300
            ||||||||||||| ||||||||||||||||||| ||||||||| |||| |||||||||||
Db   792 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCCGTGGACGTTCGGTGGA 851

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
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Db   852 GGCACCAAGCTGGAAATCAAA 872

Search completed: April 18, 2006, 18:33:15
Job time : 460 secs

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                    GenCore version 5.1.7
           Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:      April 18, 2006, 18:25:30 ; Search time 3805 Seconds
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                                        3947.084 Million cell updates/sec

Title:       US-10-764-140-1
Perfect score: 321
Sequence:    1 gacattcagatgacccagtc........ggaccaagctggagctgaaa 321

Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 1.0

Searched:    41078325 seqs, 2339354228 residues

Total number of hits satisfying chosen parameters:     82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
             1: gb_est1:*
             2: gb_est2:*
             3: gb_est3:*
             4: gb_htc:*
             5: gb_est4:*
             6: gb_est5:*
             7: gb_est6:*
             8: gb_est7:*
             9: gb_gss1:*
            10: gb_gss2:*
            11: gb_gss3:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	270.8	84.4	700	10	AG319984	AG319984 Mus muscu
2	248.2	77.3	553	2	BE309991	BE309991 601091717
3	237	73.8	603	2	CF111270	CF111270 Shultzomi
4	229.8	71.6	896	2	BG969371	BG969371 602836854
5	226.6	70.6	939	4	AK002514	AK002514 Mus muscu
6	226.6	70.6	964	2	BG966302	BG966302 602832780
7	221.8	69.1	577	2	BE305476	BE305476 601099542
8	221.8	69.1	721	2	BG967689	BG967689 602833496
9	221.2	69.1	797	6	CB987347	CB987347 AGENCOURT
10	221.2	68.9	727	9	BZ120378	BZ120378 CH230-317
11	220.2	68.6	599	2	BE287315	BE287315 601093986
12	220.2	68.6	683	6	CB984699	CB984699 AGENCOURT
13	220.2	68.6	691	2	BE307937	BE307937 601096061
14	220.2	68.6	829	7	CO575799	CO575799 AGENCOURT
15	220.2	68.6	867	2	BG754732	BG754732 602714301
16	218.6	68.1	422	1	AW407904	AW407904 UI-HF-BL0
17	218.6	68.1	472	6	CD702614	CD702614 EST19139
18	218.6	68.1	525	3	BP422398	BP422398 BP422398
19	218.6	68.1	550	6	CD709957	CD709957 EST26484
20	218.6	68.1	588	6	CD709469	CD709469 EST25996
21	218.6	68.1	616	6	CD709768	CD709768 EST26295
22	218.6	68.1	697	6	CD699896	CD699896 EST16420
23	218.6	68.1	805	3	BI454240	BI454240 603170666
24	218.6	68.1	823	2	BF580331	BF580331 602097072
25	217.2	67.7	754	2	BG967635	BG967635 602833433
26	217	67.6	431	1	AW406886	AW406886 UI-HF-BL0
27	217	67.6	460	1	AW405906	AW405906 UI-HF-BL0
28	217	67.6	465	1	AJ548351	AJ548351
29	217	67.6	493	1	AW405753	AW405753 UI-HF-BL0
30	217	67.6	499	6	CD685478	CD685478 EST1998 h
31	217	67.6	522	3	BP421572	BP421572 BP421572
32	217	67.6	568	6	CD710582	CD710582 EST27109
33	217	67.6	693	6	CD684441	CD684441 EST961 hu
34	217	67.6	724	6	CB959008	CB959008 AGENCOURT
35	217	67.6	743	6	CB957909	CB957909 AGENCOURT
36	217	67.6	769	6	CB957759	CB957759 AGENCOURT
37	217	67.6	793	6	CB987506	CB987506 AGENCOURT
38	217	67.6	799	6	CB984750	CB984750 AGENCOURT
39	217	67.6	842	6	CB986591	CB986591 AGENCOURT
40	217	67.6	886	2	BG756818	BG756818 602710291
41	217	67.6	933	2	BG533956	BG533956 602553057
42	217	67.6	1100	6	BF663472	BF663472 602144635
43	215.4	67.1	471	6	CD702236	CD702236 EST18760
44	215.4	67.1	495	6	CD708794	CD708794 EST25321
45	215.4	67.1	574	6	CD710508	CD710508 EST27035

ALIGNMENTS

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AG319984
LOCUS       AG319984                 700 bp    DNA     linear   GSS 18-DEC-2004
DEFINITION  Mus musculus molossinus DNA, clone:MSMg01-105L04.T7, genomic survey
            sequence.
ACCESSION   AG319984
VERSION     AG319984.1  GI:47892941
KEYWORDS    GSS.
SOURCE      Mus musculus molossinus (Japanese wild mouse)
  ORGANISM  Mus musculus molossinus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
            Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
            Shiroishi,T.
  TITLE     Contribution of Asian mouse subspecies Mus musculus molossinus to
            genomic constitution of strain C57BL/6J, as defined by BAC-end
            sequence-SNP analysis
  JOURNAL   Genome Res. 14 (12), 2439-2447 (2004)
  PUBMED    15574823
REFERENCE   2  (bases 1 to 700)
  AUTHORS   Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
            (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the mouse BAC library MSMg01. For BAC
            library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
            Tsukuba Institude, Bio Resource Center,
            The Institute of Physical and Chemical Research (RIKEN) 3-1-1
            Koyadai, Tsukuba, 305-0074 Japan
            phone: 81-298-36-9189, fax: 81-298-36-9199
            e-mail: abe@rtc.riken.jp
            PRIMERS
            Sequencing : T7
            LIBRARY
            Vector      : pBACe3.6
            R.Site 1    : EcoRI
            R.Site 2    : EcoRI.
FEATURES             Location/Qualifiers
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                        /clone_lib="NCI_CGAP_Mam5"
                        /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                        Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                        Library constructed by Life Technologies. Investigators
                        providing samples: Lothar Hennighausen/Robin Humphreys,
                        NIH"

ORIGIN

       Query Match           77.3%;   Score 248.2;  DB 2;   Length 553;
       Best Local Similarity  93.2%;  Pred. No. 1.9e-65;
       Matches  303;  Conservative  0;  Mismatches  18;  Indels  4;  Gaps  4;

Qy      1 GACATTCAGATGACCCAG-TCTCCTGCCTCCCAGTCCATCTCTGGGAGAAAGTGTCAC  59
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Db     46 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCCATCTCTGGGAGAAAGTGTCAC  105

Qy     60 CA-TCACATGCCTGGCAAGTCAGACCATTGATACA-TGGTTAGCATGGTATCAGCAGAAA  117
          || ||||||||||||||||||||||||||||| || |||||||||||||||||||||||
Db    106 CAGTCACATGCCTGGCAAGTCAGACCATTGTACACTGGTTAGCATGGTATCAGCAGAAA  165

Qy    118 CCAGGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCA  177
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Db    166 CCAGGGAAATCTCCTCAACTCCTGATTTATGCTGCCAGCCAGTTGCAGATGGGGTCCCA  225

Qy    178 TCAAGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTCAAGATCAGCAGCCTACAG  237
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Db    226 TCAAGGTTCAGTGGTGTGGATCTGGCACAAAATTTTCTTCAAGATCAGCAGCCTACAG  285

Qy    238 GCTGAAGATTTTGTAAATTATTACTGTCAACAA-GTTTACAGTTCTCCATTCACGTTCGG  296
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Db    286 GCTGAAGATTTTGTAACTTATTACTGTCAACAACGTTTACAGTACTCCGTGGACGTTCGG  345

Qy    297 TGCTGGGACCAAGCTGGAGCTGAAA  321
          ||||| ||||||||||||||| |||
Db    346 TGGAGGCACCAAGCTGGAAATCAA  370


RESULT 3
CF111270
LOCUS           CF111270                  603 bp    mRNA      linear   EST 23-JUL-2003
DEFINITION      Shultzomica04521 Rat lung airway and parenchyma cDNA libraries
                Rattus norvegicus cDNA clone Contig432 5', mRNA sequence.
ACCESSION       CF111270
VERSION         CF111270.1  GI:33167972
KEYWORDS        EST.
SOURCE          Rattus norvegicus (Norway rat)
  ORGANISM      Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE       1  (bases 1 to 603)
  AUTHORS       Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
                Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
                Plopper,C.G. and Buckpitt,A.R.
  TITLE         Gene expression analysis in response to lung toxicants: I.
                Sequencing and microarray development
  JOURNAL       Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
  PUBMED        12947022
  COMMENT       Contact: Shultz MA
                Dept. of Molecular Biosciences, School of Veterinary Medicine
                University of California, Davis
                1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
                Tel: 530 752 0793
                Fax: 530 752 4698
                Email: mashultz@ucdavis.edu
                Average Phred score is 20 or better. All poor quality data (Phred <
                20) and vector/linker sequence has been removed.
                High quality sequence stop: 603.
FEATURES             Location/Qualifiers
     source          1..603
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
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                        /organism="Mus musculus molossinus"
                        /mol_type="genomic DNA"
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                        /clone="MSMg01-105L04.T7"
                        /sex="male"
                        /tissue_type="mixture of kidney and spleen"
                        /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

       Query Match           84.4%;   Score 270.8;  DB 10;  Length 700;
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       Matches  278;  Conservative  0;  Mismatches  12;  Indels  0;  Gaps  0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCCATCTCTGGGAGAAAGTGTCACC  60
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Qy     61 ATCACATGCCTGGCAAGTCAGACAGCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA  120
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Db    151 ATCACATGCCTGGCAAGTCAGACAGCATTGTACATGGTTAGCATGGTATCAGCAGAAACCA  210

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
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Db    211 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCAACCAGCTTGGCAGATGGGGTCCCATCA  270

Qy    181 AGGTTCAGTGGCAGTGGATCTGGCACAGAAATTTTCTTCAAGATCAGCAGCCTACAGGCT  240
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Db    271 AGGTTCAGTGGTAGTGGATCTGGCACAGAAATTTTCTTCAAGATCAGCAGCCTACAGGCT  330

Qy    241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCAC  290
          |||||||||| ||||||||||||||||||||||||||||||||||||||
Db    331 GAAGATTTTGTCAAGTTATTACTGTCAACAACATTACAGTACTCCTCTCAC  380


RESULT 2
BE309991
LOCUS           BE309991                  553 bp    mRNA      linear   EST 26-OCT-2000
DEFINITION      601091717F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3486245 5',
                mRNA sequence.
ACCESSION       BE309991
VERSION         BE309991.1  GI:9169034
KEYWORDS        EST.
SOURCE          Mus musculus (house mouse)
  ORGANISM      Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE       1  (bases 1 to 553)
  AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
  TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL       Unpublished (1999)
  COMMENT       Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
                cDNA Library Preparation: Life Technologies, Inc.
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLAM8522 row: b column: 06
                High quality sequence start: 48
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FEATURES             Location/Qualifiers
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                                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                     Average insert size 1.75 kb. Constructed by Life
                                     Technologies. Note: this is a NCI_CGAP Library. |"
     ORIGIN

Query Match         71.6%;  Score 229.8;  DB 2;  Length 896;
Best Local Similarity   82.2%;  Pred. No. 1.1e-59;
  Matches  264;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCTCCCAGTCTGCATCTCGGGAGAAAGTGTCACC  60
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Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA  120
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Db    139 ATCACATGTCGAGCAAGTGAGAATATTTACAGTAATTAGCATGGTATCAGCAGAAACAG  198

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGAGTGGGGTCCCATCA  180
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Db    199 GGGAAAATCTCCTCAGCTCCTGGTCTATGGTGCAACAAATTTAGGAGATGGTGTGCCATCA  258

Qy    181 AGGTTCAGTGCGCAGTGGATCTGGCACAAAAATTTCTTCAAGATCAGCAGCCTACAGGCT  240
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Db    259 AGGTTCAGTGGCAGTGGATCAGGCACAGATTCCCTCAAGATTATTCACAGTCT  318

Qy    241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT  300
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Qy    301 GGGACCAAGCTGGAGCTGAAA  321
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Db    379 GGGGACCAAGGTGGAGCTGAAA  399

RESULT 5
AK002514
LOCUS       AK002514                 939 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus adult male kidney cDNA, RIKEN full-length enriched
            library, clone:0610010P20 product:immunoglobulin kappa chain
            variable 28 (V28), full insert sequence.
ACCESSION   AK002514
VERSION     AK002514.1  GI:12282550
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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                                    /clone_lib="Rat lung airway and parenchyma cDNA libraries"
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                                     lung airways and parenchyma tissues."
     ORIGIN

Query Match         73.8%;  Score 237;  DB 6;  Length 603;
Best Local Similarity   85.4%;  Pred. No. 5.9e-62;
  Matches  275;  Conservative    0;  Mismatches   46;  Indels    1;  Gaps    1;

Qy      1 GACATTCAGATGACCCAGTCTCCT-GCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCAC  59
          |||||||||||||| |||||||||  |||||||||||| |||| ||||||||| |||||
Db     41 GACATCCAGATGACACAGTCTCCTGCCTCCCCTGTCTGCCTCCCTGGAAGAAAATTGTCAC  100

Qy     60 CATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACC  119
          |||||||||| |||| || ||||||||| | ||  || | |||||||||||||||||||
Db    101 GATCACATGCCAGGCAAGCCAGGACATTGGTAATTGGTTAACATGGTATCAGCAGAAACC  160

Qy    120 AGGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATC  179
          ||||||||||||||||||| |||| || ||| |||||| ||||||| |||||||||||||
Db    161 AGGNAAATCTCCTCAGCTCCTGATCTCATGGTGCAACCAGCTTGGCAGATGGGGTCCCATC  220

Qy    180 AAGGTTCAGTGGCAGTGGATCTGGCACAAAAATTTCTTCAAGATCAGCAGCCTACAGGC  239
          |||||||||||||| |||||||||||  |||||| ||||||| |||||||||||||||||
Db    221 AAGGTTCAGTGGCAGTGGATCTGGCACAGATCTCTCAAGATCAGCAGACTACAGGT  280

Qy    240 TGAAGATTTTGTAAATTATTACTGTCAACAAGTTTCCATTCACGTTCGGTGC  299
          ||||||||| | |||| || ||||||  |||||| || |||||||||||||
Db    281 TGAAGATCCTGGAATCTATTACTGTCTACAGAGTTATAGTACTCCCGGACGTTCGGTGG  340

Qy    300 TGGGACCAAGCTGGAGCTGAAA  321
          ||||||||||||||||||||||
Db    341 AGGCACCAAGCTGGAATTGAAA  362

RESULT 4
BG969371
LOCUS       BG969371                 896 bp    mRNA    linear   EST 12-JUN-2001
DEFINITION  602836854F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4971397
            5', mRNA sequence.
ACCESSION   BG969371
VERSION     BG969371.1  GI:14357008
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10956 row: k  column: 14
            High quality sequence stop: 864.
FEATURES             Location/Qualifiers
     source          1..896
                     /organism="Mus musculus"
                     /mol_type="mRNA"
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TITLE              Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                   RIKEN integrated sequence analysis (RISA) system--384-format
                   sequencing pipeline with 384 multicapillary sequencer
JOURNAL            Genome Res. 10 (11), 1757-1771 (2000)
PUBMED             11076861
REFERENCE          4
AUTHORS            The RIKEN Genome Exploration Research Group Phase II Team and the
                   FANTOM Consortium.
TITLE              Functional annotation of a full-length mouse cDNA collection
JOURNAL            Nature 409, 685-690 (2001)
REFERENCE          5
AUTHORS            The FANTOM Consortium and the RIKEN Genome Exploration Research
                   Group Phase I & II Team.
TITLE              Analysis of the mouse transcriptome based on functional annotation
                   of 60,770 full-length cDNAs
JOURNAL            Nature 420, 563-573 (2002)
REFERENCE          6 (bases 1 to 939)
AUTHORS            Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
                   Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
                   Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
                   Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
                   Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
                   Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
                   Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
                   Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
                   Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
                   Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
                   Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
                   Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE              Direct Submission
JOURNAL            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                   Physical and Chemical Research (RIKEN), Laboratory for Genome
                   Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                   RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                   Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
                   URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9216,
                   Fax:81-45-503-9222)
COMMENT            Please visit our web site (http://genome.gsc.riken.jp/) for further
                   details.
                   cDNA library was prepared and sequenced in Mouse Genome
                   Encyclopedia Project of Genome Exploration Research Group in Riken
                   Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                   Division of Experimental Animal Research in Riken contributed to
                   prepare mouse tissues. First strand cDNA was primed with a primer
                   [5' GAGAGAGAGAGAGCGGGGCCCCAACTCGAGTTTTTTTTTTTTTTVN 3'], cDNA was
                   prepared by using trehalose thermo-activated reverse transcriptase
                   and subsequently enriched for full-length by cap-trapper. cDNA went
                   through one round of normalization to Rot = 5.0. Second strand cDNA
                   was prepared with the primer adapter of sequence[5'
                   GAGAGAGAGGAGATCCAAGAGCTCAATTAATTTAATTAAACCCCCCCCCC 3']. cDNA was
                   cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
                   XhoI. Host: SOLR.
FEATURES           Location/Qualifiers
     source        1..939
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="C57BL/6J"
                   /db_xref="FANTOM_DB:0610010P20"
                   /db_xref="taxon:10090"
                   /clone="0610010P20"
                   /sex="male"
                   /tissue_type="kidney"
                   /clone_lib="RIKEN full-length enriched mouse cDNA library"
                   /dev_stage="adult"
     CDS           101..736
                   /note="unnamed protein product; immunoglobulin kappa chain
                   variable 28 (V28) (LocusLink|16114, GB|AK002514, evidence:
                   BLASTN, 100%, match=939)
                   /codon_start=1
                   /product="putative"
                   /protein_id="BAB22154.1"
                   /db_xref="GI:12832551"
                   /translation="MTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKGKSPQLL
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                   IKRADAPTVSIFPPSSEQLTSGGASVVCFLNFYPKDINVKWKIDGSERQNGVLNSW
                   TDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC"
polyA_signal       922..927
                   /note="putative"
polyA_site         939
                   /note="putative"
ORIGIN

Query Match         70.6%;  Score 226.6;  DB 4;  Length 939;
Best Local Similarity  81.6%;  Pred. No. 1.1e-58;
Matches  262;    Conservative   0;  Mismatches  59;  Indels  0;  Gaps  0;

Qy          1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         92 GACATCCAGATGACTCAGTCTCCAGCTCCCTATCTGTATCTGTGGGAGAAACTGTCACC 151

Qy         61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATCAGCAGAAACCA 120
              |||||||| ||||||| ||||| ||  ||||||||| |||||||||||||||||||||
Db        152 ATCACATGTCGAGCAAGTGAGAATATTTACAGTAATTTAGCATGGTATCAGCAGAAACAG 211

Qy        121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
              |||||||||||||||||||||| |||||||| || |||||| || ||||||||| ||||||
Db        212 GGAAAATCTCCTCAGCTCCTGGTCTATGCTGCCAACAAACTTAGCAGATGGTGTGCCATCA 271

Qy        181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
              |||||||||||||||||||||||||| ||||| |||| |||||||||| |||||||||||||
Db        272 AGGTTCAGTGGCAGTGGATCAGGCACACAGATTATTCCCTCAAGATCAACAGCCTGCAGTCT 331

Qy        241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
              |||||||| |||   ||| ||||||||||| |||| ||||||||||||||||||||||||
Db        332 GAAGATTTTGGGAGTTATTCTGTCAACATTTTGGGGTACTCCTCGGACGTTCGGTGGA 391

Qy        301 GGGACCAAGCTGGAGCTGAAA 321
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Db        392 GGCACCAAGCTGGGAGATCAAA 412
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RESULT 6
BG966302
LOCUS       BG966302              964 bp    mRNA     linear    EST 12-JUN-2001
DEFINITION  602837780F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4987626 5',
            mRNA sequence.
ACCESSION   BG966302
VERSION     BG966302.1  GI:14353939
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 964)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10998 row: o  column: 19
            High quality sequence stop: 826.
FEATURES           Location/Qualifiers
     source        1..964
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="FVB/N"
                   /db_xref="taxon:10090"
                   /clone="IMAGE:4987626"
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                    /lab_host="DH10B (T1 phage-resistant)"
                    /clone_lib="NCI_CGAP_Co24"
                    /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                    Average insert size 1.6 kb. Constructed by Life
                    Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

Query Match        70.6%;   Score 226.6;  DB 2;   Length 964;
Best Local Similarity  81.6%;  Pred. No. 1.1e-58;
Matches 262;  Conservative  0;  Mismatches  59;  Indels  0;  Gaps  0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
        ||||| |||||||||||||||||| |||| |||| |||||||||||||||||||||||||
Db  76 GACATCCAGATGACTCAGTCTCCCAGCCTCCTATCTGTGTGGGAGAAACTGTCACC 135

Qy  61 ATCACATGCCTGGCAAGTCAGACCATTGATGACAGTGTTAGCAGTGTATCAGCAGAAACCA 120
        ||||||||| |||||||||||  |||| ||||||| ||||||||||||| |||||||||||
Db 136 ATCACATGTCAGCAAGTGAGAATATTTACAGTAATTTAGCAGTGTATCAGCAGAAACAG 195

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
        |||||||||||||||||||||| ||| ||||| |||||||| |||||||| ||||||||
Db 196 GGGAAATCTCCTCAGCTCCTGGTCTATGGTGCAACAAACTTAGCAGATGGTGTGCCATCA 255

Qy 181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
        |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||| |
Db 256 AGGTTCAGTGGCAGTGGATCGGGACACAGTATTCCCTCAAGATCAACAGCCTGCAGTCT 315

Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
        |||||||| ||||||||||||||||||||||  |||  |||||||||||||||||||||
Db 316 GAAGATTTTGGAATTATTTCTGTCAACATTTTTGGGGTACTCCGTGGACGTTCGGTGGA 375

Qy 301 GGGACCAAGCTGGAGCTGAAA 321
        || |||||||||||||||||
Db 376 GGCACCAAGCTGGAAATCAAA 396


RESULT 7
BE305476
LOCUS       BE305476          577 bp   mRNA    linear    EST 26-OCT-2000
DEFINITION  601099542F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3492034 5',
            mRNA sequence.
ACCESSION   BE305476
VERSION     BE305476.1  GI:9157223
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 577)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8537 row: c  column: 11
            High quality sequence stop: 576.
FEATURES             Location/Qualifiers
     source          1..577
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="Czech II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3492034"
                     /tissue_type="spontaneous tumor, metastatic to mammary.
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                    Stem cell origin."
                    /lab_host="DH10B"
                    /clone_lib="NCI_CGAP_Lu29"
                    /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
                    Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                    Library constructed by Life Technologies. Investigator
                    providing samples: Gilbert Smith, NIH"
ORIGIN

Query Match        69.1%;   Score 221.8;  DB 2;   Length 577;
Best Local Similarity  80.7%;  Pred. No. 3e-57;
Matches 259;  Conservative  0;  Mismatches  62;  Indels  0;  Gaps  0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db  56 GACATCCAGATGACTCAGTCTCCAGCCTCTCTATCTGCATCTGTGGGAGAAACTGTCACC 115

Qy  61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCAGTGTATCAGCAGAAACCA 120
        ||||||||| |||||||||||  |||| || | |  ||||||||||| ||||||||||
Db 116 ATCACATGTCGAGCAAGTGAGAATATTTACAGTTATTTAGCATGGTATCAGCAGAAACAG 175

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
        |||||||||||||||||||||| ||| ||||| |||||||| |||||||| ||||||||
Db 176 GGAAAATCTCCTCAGCTCCTGGTCTATAATGCAACAAAACCTTAGCAGAGAGGGTGCCATCA 235

Qy 181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
        ||||||||||||||||||||| ||||||||| ||| ||||||||||||||||||||
Db 236 AGGTTCAGTGGCAGTGGATCAGGGACACCAGTTTCTGAGATCAACAGCCTGCAGCCT 295

Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db 296 GAAGATTTTGGAGTTATTATTACTGTCAACATCATTATGGTACTCCTCCGACGTTCGGTGGA 355

Qy 301 GGGACCAAGCTGGAGCTGAAA 321
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Db 356 GGCACCAAGCTGGAAATCAAA 376


RESULT 8
BG967689
LOCUS       BG967689          721 bp   mRNA    linear    EST 12-JUN-2001
DEFINITION  602833496F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988038 5',
            mRNA sequence.
ACCESSION   BG967689
VERSION     BG967689.1  GI:14355326
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 721)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1099 row: p  column: 23
            High quality sequence stop: 720.
FEATURES             Location/Qualifiers
     source          1..721
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4988038"
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                    /lab_host="DH10B (T1 phage-resistant)"
                    /clone_lib="NCI_CGAP_Co24"
                    /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                    Average insert size 1.6 kb. Constructed by Life
                    Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match   69.1%;   Score 221.8; DB 2; Length 721;
Best Local Similarity   80.7%;   Pred. No. 3.2e-57;
Matches 259; Conservative   0; Mismatches 62; Indels   0; Gaps   0;

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Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCGCATCTCTGGGAGAAAGTGTCACC   60
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Db   81 GACATCCAGATGACTCAGTCTCCATCCTCCCTATCTGCATCTGTGTGGGAGAAACTGTCACC  140

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA  120
         ||||  || | ||||||| |||| |||||||||||||||||||| | |||||||||||||
Db  141 ATCATATGTCGAGCAAGTGAGAATATTTACAGTTATTTAGCATGCATGTATCAGCAGAAACAG  200

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
         ||||||||| ||||||||| | | |||  |  |  |  || ||| || |||||||||||
Db  201 GGGAAAATCTTCCTCAGCTCCGTCTATAATGCAAAAACCTTAGGAGAAGTGTGCCATCA  260

Qy  181 AGGTTCAGTGGCAGTGGATCTGGGACAAAAATTTTCTTCAAGATCAGCAGCCTACAGGCT  240
         |||||||||||||||||| | ||||||| | ||||| |||||||||| ||||| ||| |
Db  261 AGGTTCAGTGGCAGTGGAATCAGGCACCACAGTTTTCTCTGAAGATCAACAGCCTGCAGCCT  320

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT  300
         |||||||||| | |||||||||||||||| | |||||||| ||||||||||||||| | |
Db  321 GAAGATTTTGCGGAGTTATTACTGTCAACAGCATTATGGTACTCCATTCACGTTCGGCTCG  380

Qy  301 GGGACCAAGCTGGAGCTGAAA  321
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Db  381 GGGACCAAGTTGGAAATAAAA  401
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RESULT 9
CB987347
LOCUS   CB987347   797 bp   mRNA   linear   EST 01-MAY-2003
DEFINITION AGENCOURT 13591809 NIH_MGC_184 Homo sapiens cDNA clone
            IMAGE:30326300 5', mRNA sequence.
ACCESSION   CB987347
VERSION   CB987347.1 GI:30281867
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 797)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM133 row: h column: 21
            High quality sequence stop: 437.
FEATURES   Location/Qualifiers
     source   1..797
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30326300"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_184"

                    /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
                    SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc);
                    Library is oligo-dT primed and directionally cloned. cDNA
                    was prepared from a glandular pool of tissues from thyroid,
                    parathyroid, adrenal, cortex and pineal gland. 5' and 3'
                    adaptors were used in cloning as follows: 5' adaptor
                    sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                    5'-ATTCTAGAGCCGAGGCGGCGGACGAATG-dT(30)BN-3' (where B = A,
                    C, or G and N = A, C, G, or T). Average insert size 1.38
                    kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
                    by PCR. This library was enriched for full-length clones
                    and was constructed by Clontech Laboratories (Palo Alto,
                    CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match   69.1%;   Score 221.8; DB 6; Length 797;
Best Local Similarity   80.7%;   Pred. No. 3.3e-57;
Matches 259; Conservative   0; Mismatches 62; Indels   0; Gaps   0;

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Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCGCATCTCTGGGAGAAAGTGTCACC   60
         ||||| |||||||||||||||||| ||| ||  | ||||||||   ||| || || ||||
Db   99 GACATCCAGATGACCCAGTCTCCATCTCCCGTCTGCATCTGTGTAGGAGACAGAGTCACC  158

Qy   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA  120
         |||||  ||| | ||||||||| |||| | | | | || || |||||||||||||||||
Db  159 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGTGCTTTAAATTGGTATCAGCAGAAACCA  218

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
         ||||||  || |||||||||||| |||| |||| |  | |||| |  |||||||||||||
Db  219 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA  278

Qy  181 AGGTTCAGTGGCAGTGGATCTGGGACAAAAATTTTCTTCAAGATCAGCAGCCTACAGGCT  240
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Db  279 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACCT  338

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT  300
         ||||||||||  | | | |||||||||  | |||||||||| |||||||| |||||  | |
Db  339 GAAGATTTTGCAACTTACTACTGCCAAGAGACTTACAGTTCCCATTCACTTTCGGCCCT  398

Qy  301 GGGACCAAGCTGGAGCTGAAA  321
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Db  399 GGGACCAAAGTGGATATCAAA  419
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RESULT 10
BZ120378
LOCUS   BZ120378   727 bp   DNA   linear   GSS 11-OCT-2002
DEFINITION CH230-317B9.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
            CH230-317B9, genomic survey sequence.
ACCESSION   BZ120378
VERSION   BZ120378.1 GI:23761125
KEYWORDS   GSS.
SOURCE   Rattus norvegicus (Norway rat)
  ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 727)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE   Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT   Other_GSSs: CH230-317B9.TJ
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.html). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 317 row: B column: 9
Seq primer: T7
Class: BAC ends.

FEATURES   Location/Qualifiers
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                  /mol_type="genomic DNA"
                  /strain="BN/SsNHsd/MCW"
                  /db_xref="taxon:10116"
                  /clone="CH230-317B9"
                  /sex="Female"
                  /cell_type="Brain"
                  /clone_lib="CHORI-230 Segment 2"
                  /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                  CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                  Pieter de Jong"

ORIGIN

Query Match   68.9%;   Score 221.2;   DB 9;   Length 727;
Best Local Similarity 85.2%;   Pred. No. 4.9e-57;
Matches 247; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db   83 GACATCCAGATGACACAGTCTCAGTCTCCAGCCTCCTGTCTGCATCTCTGGGAGAAATTGTCACC 142

Qy   61 ATCACATGCCTGGCAAGTCAGCCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db 143 ATCACATGCCAGGCAAGCCTGGACATTGGTAATTGGTTAGCATGGTATCAGCAGAGAAACCA 202

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCATCA 180
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Db 203 GGGAAATCTCCTCAGCTCCTGATCTATGGTGCCAACCAGCGTTGGCAGATGGGGTCCATCA 262

Qy 181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
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Db 263 AGGTTCAGCGGCAGTAGATCTGGCACACAGCAGTATTCCTTAAGATCTTGCAAACTACAGGTT 322

Qy 241 GAAGATTTTGTAAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCAC 290
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Db 323 GAAGATACTGGAATCTATTACTGTCTACAGCATTATAGTGTCTCCTCCCAC 372

RESULT 11
BE287315
LOCUS   BE287315   599 bp   mRNA   linear   EST 26-OCT-2000
DEFINITION   601093986F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3488780 5',
               mRNA sequence.
ACCESSION   BE287315
VERSION   BE287315.1   GI:9166132
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 599)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov

Plate: LLAM8528 row: k column: 21
High quality sequence stop: 542.
                  Location/Qualifiers
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                  /organism="Mus musculus"
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FEATURES   Location/Qualifiers
  source   1..599
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                  /mol_type="mRNA"
                  /strain="mix FVB/N, C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="IMAGE:3488780"
                  /tissue_type="tumor, gross tissue"
                  /dev_stage="7 months"
                  /lab_host="DH10B"
                  /clone_lib="NCI_CGAP_Mam5"
                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                  Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                  Library constructed by Life Technologies. Investigators
                  providing samples: Lothar Hennighausen/Robin Humphreys,
                  NIH."

ORIGIN

Query Match   68.8%;   Score 220.2;   DB 2;   Length 599;
Best Local Similarity 80.4%;   Pred. No. 9.4e-57;
Matches 258; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db   67 GACATCCCAGATGACTCAGTCTCCAGCCTCCTATCTGTCTCTGTGGGGAGAAAACTGTCACC 126

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db 127 ATCACATGTCGAGCAAGTGAAAATATTTACAGTAATTTAGCATGGTATCAGCAGAAACAG 186

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCATCA 180
         |||||||||||||||||||||| || |||||||||||||||||||||||||||||||
Db 187 GGGAAATCTCCTCAGCTCCTGGTCTATGCTGCCAACAACTTAGCAGATGGTGTGCCATCA 246

Qy 181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
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Db 247 AGATTCAGTGGCAGTGGATCAGCAGCACAGTATTCCCTCACGATTATCCCACGATCAACAGCCTGCAGTCT 306

Qy 241 GAAGATTTTGTAAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCGGTGCT 300
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Db 307 GAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGGGTACTCGTTCACATTCGGAGGG 366

Qy 301 GGGACCAAGCTGGAGCTGAAA 321
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Db 367 GGGACCAAAGTGGGGGATAAAA 387

RESULT 12
CB984699
LOCUS   CB984699   683 bp   mRNA   linear   EST 01-MAY-2003
DEFINITION   AGENCOURT_13460627 NIH_MGC_184 Homo sapiens cDNA clone
               IMAGE:30325948 5', mRNA sequence.
ACCESSION   CB984699
VERSION   CB984699.1   GI:30279223
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1 (bases 1 to 683)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
               cDNA Library Preparation: CLONTECH Laboratories, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be

COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA Library Preparation: Lothar Hennighausen Ph.D., Robin Humphreys
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM533 row: i column: 16
            High quality sequence stop: 568.
FEATURES   Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="mix FVB/N, C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:3490647"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="7 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam5"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectional; Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Robin Humphreys,
                     NIH."
ORIGIN

     Query Match   68.6%;   Score 220.2;   DB 2;   Length 691;
     Best Local Similarity 80.4%;   Pred. No. 9.8e-57;
     Matches 258;   Conservative   0;   Mismatches 63;   Indels   0;   Gaps   0;

     Qy   1 GACATTCAGATGACGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
              |||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
     Db   72 GACATTCCAGATGACTCAGTCTCCAGTCCTCCCATCTGTATCTGTGTGGGAGAAACTGTCACC 131

     Qy   61 ATCACATGCCTGGCAAGTCAGACCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
              ||||||| | ||||||||||||||||||| |||||||||||||||||||||||||||||||
     Db 132 ATCACATGTCGAACAAGTGAGAATATTTACAGTAATTTAGCATGGTATCAGCAGAAACAG 191

     Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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     Db 192 GGGAAATCTCCTCAGCTCCTGGTCTGTCTATGCTGCCAACAAACTTAGCAGAGACGGGTGTGCCATCA 251

     Qy 181 AGGTTCAGTGGCAGTGGATCTGGACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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     Db 252 AGGTTCAGTGGCAGTGGATCAGGCACAGTATTCACTAACGATCAACAGCCTGCAGTCT 311

     Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTCACATTTTGGGGTACTCCGTTCGGTGCT 300
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     Db 312 GAAGATTTTCAACATTTTCAACATTTTGGGGTACTCCGTACACGTTCGGAGGG 371

     Qy 301 GGGACCAAGCTGGAGCTGAAA 321
              |||||||||||||||||||||
     Db 372 GGGACCAAGCTGGGAATAAAA 392

RESULT 14
CO575799
LOCUS   CO575799   829 bp   mRNA   linear   EST 19-JUL-2004
DEFINITION AGENCOURT 28538931 NIH_MGC 249 Rattus norvegicus cDNA clone
            IMAGE:7375130 5', mRNA sequence.
ACCESSION   CO575799
VERSION   CO575799.1 GI:50388428
KEYWORDS   EST.
SOURCE   Rattus norvegicus (Norway rat)
  ORGANISM Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 829)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.

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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM132 row: j column: 05
High quality sequence stop: 547.
     Location/Qualifiers
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          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="IMAGE:3032948"
          /lab_host="DH10B (T1 phage-resistant)"
          /clone_lib="NIH_MGC_184"
          /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
          SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc);
          Library is oligo-dT primed and directionally cloned. cDNA
          was prepared from a glandular pool of tissues from thyroid,
          parathyroid, adrenal, cortex and pineal gland. 5' and 3'
          adaptors were used in cloning as follows: 5' adaptor
          sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
          5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
          C, or G and N = A, C, G, or T). Average insert size 1.38
          kb (range 0.60-3,5 kb). 15/15 colonies contained inserts
          by PCR. This library was enriched for full-length clones
          and was constructed by Clontech Laboratories (Palo Alto,
          CA). Note: this a NIH_MGC Library."
ORIGIN

     Query Match   68.6%;   Score 220.2;   DB 6;   Length 683;
     Best Local Similarity 80.4%;   Pred. No. 9.8e-57;
     Matches 258;   Conservative   0;   Mismatches 63;   Indels   0;   Gaps   0;

     Qy   1 GACATTCAGATGACGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
              |||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
     Db   90 GACATTCCAGATGACCCAGTCTCCATCCTCCTGTCTGCATCTATAGGAGACAGAGTCACC 149

     Qy   61 ATCACATGCCTGGCAAGTCAGACCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
              ||||||| | ||||||||||||||||||| ||||||||||||||||||||||||||| |||
     Db 150 ATCACTTGCCGGGCCAGTCAGGGCATTAGCAGTTATTTAGCCTGGTATCAGCAGAAAATCA 209

     Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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     Db 210 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 269

     Qy 181 AGGTTCAGTGGCAGTGGATCTGGACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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     Db 270 AGGTTCAGCGGCGGTGGATCTGGGACAGAGTTCACTCTCACACTCAGCAGCCTGCAGCCT 329

     Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTCACATTTTGGGGTACTCCGTTCGGTGCT 300
              ||||||||| | ||||||||||||||||||||| |||||||||||||||||||||||||
     Db 330 GAAGATTTTGCAACTTATTACTGTCAACAACTTTACAGTTACCCTTTCACTTTCGGCGGA 389

     Qy 301 GGGACCAAGCTGGAGCTGAAA 321
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     Db 390 GGGACCAGGGTGGAGATCAAA 410

RESULT 13
BE307937
LOCUS   BE307937   691 bp   mRNA   linear   EST 26-OCT-2000
DEFINITION 601096061F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3490647 5',
            mRNA sequence.
ACCESSION   BE307937
VERSION   BE307937.1 GI:9163812
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 691)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)

```
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact:Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
            College of Wisconsin
            cDNA Library Preparation: Open Biosystems
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15525 row: b  column: 24
            High quality sequence stop: 632.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7375130"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC 249"
                     /note="Organ: spleen; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from testis tissue of 8 wk old
                     animal. Tissues were snap-frozen and kept at -80C before
                     RNA extraction and purification (Tri-reagent method). cDNA
                     was primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGGCAGCGAGGCGGCCGCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
                     resulted in an average insert size of 1.4 kb. This primary
                     library is normalized ( primary library is NIH_MGC_248)
                     and was constructed by Express Genomics (Frederick, MD).
                     Note: this is a NIH_MGC library"
ORIGIN

Query Match             68.6%;  Score 220.2;  DB 7;  Length 829;
Best Local Similarity   80.4%;  Pred. No. 1e-56;
Matches   258;  Conservative   0;  Mismatches  63;  Indels   0;  Gaps   0;

Qy          1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
              |||||| |||||||| |||||||| || ||||| |||||||||||| ||||||| ||| ||
Db         71 GACATCCAGATGACACAGTCTCCAGCTTCCCTGTCTGCATCTCTTGGAGAAACTGTCTCC 130

Qy         61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
              ||| || |||| ||||||| ||  |||| | ||| | ||||| |||||||||||||| |
Db        131 ATCGAAATGTCTAGCAAGTGAGGGCATTTCCAATGATTTAGCGTGGTATCAGCAGAAGTCA 190

Qy        121 GGGAAATCTCCTCAGCTCCTGATTTATGTGCCACCAACTTGGCAGATGGGTCCCATCA 180
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Db        191 GGGAAATCTCCTCAGCTCCTGATCTATGTGCAAGTAGGTTGCAAGACCGGGTCCCATCA 250

Qy        181 AGGTTCAGTGGCAGTGGATCTGGGCACAGATCAGCAGCCTACAGGCT 240
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Db        251 CGGTTCAGTGGCAGTGGATCTGGGCACAGATTTCTCAAGATCAGCAGCCTGCAACCT 310

Qy        241 GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTTACAGTTTCTCCATTCACGTTCGGTGCT 300
              |||||| |   ||||| |||||||||||| |||  ||||| | ||||  |||| |||| |||||
Db        311 GAAGATGAAGCAGATTATTTCTGTCAACAGAGTTACAACAGTATCCGTACACGTTTGGAGCT 370

Qy        301 GGGACCAAGCTGGAGCTGAAA 321
              |||||||||||||| ||||||
Db        371 GGGACCAAGCTGGAACTGAAA 391

RESULT 15
BG754732
LOCUS       BG754732      867 bp    mRNA      linear   EST 15-MAY-2001
DEFINITION  602714301F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854409 5',
            mRNA sequence.
ACCESSION   BG754732
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VERSION     BG754732.1  GI:14065385
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 867)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1702 row: a  column: 02
            High quality sequence stop: 805.
FEATURES             Location/Qualifiers
     source          1..867
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4854409"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC 48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

Query Match             68.6%;  Score 220.2;  DB 2;  Length 867;
Best Local Similarity   80.4%;  Pred. No. 1.1e-56;
Matches   258;  Conservative   0;  Mismatches  63;  Indels   0;  Gaps   0;

Qy          1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCGCATCTCTGGGAGAAAGTGTCACC 60
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Db         85 GCCATCCAGTTGACCCAGTCTCCAGCTTCCCTGTCTGCATCTCTGTGTAGGAGACAGAGTCACC 144

Qy         61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
              ||| |||| | | |||||||| |||  || | ||| | ||  ||||||||||||||| ||
Db        145 ATCACTTGCCGGGCAAGTCAGGCCATTAGCAGTGCTTAGCCTGGTATCAGCAGAAACCA 204

Qy        121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
              |||||| |||| ||||||||||| |||| ||| || | |||||| ||||| ||||| ||||
Db        205 GGGAAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTGTTGGGAAAGTGGGGTCCCCTCA 264

Qy        181 AGGTTCAGTGGCAGTGGATCTGGGCACAGATCAGCAGCCTACAGGCT 240
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Db        265 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 324

Qy        241 GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTTACAGTTTCACGTTCGGTGCT 300
              |||||||||| ||  ||||||||||||| ||| ||| | || |||| ||| |||| |
Db        325 GAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAATTACCCTCCACTTTCGGCGGA 384

Qy        301 GGGACCAAGCTGGAGCTGAAA 321
              ||||||||| |||||  |  ||
Db        385 GGGACCAAGGTGGAGATCAAA 405
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Search completed: April 18, 2006, 20:05:21
Job time : 3808 secs

GenCore version 5.1.7

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 18:26:07 ; Search time 167 Seconds
                          (without alignments)
                          3416.750 Million cell updates/sec

Title: US-10-764-140-1
Perfect score: 321
Sequence: 1 gacattcagatgaccagtc.........ggaccaagctggagctgaaa 321

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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                2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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                5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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                8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	321	100.0	321	2	US-08-814-806-1	Sequence 1, Appli
2	321	100.0	321	2	US-09-293-854-1	Sequence 1, Appli
3	293.8	91.5	375	3	US-09-647-468-12	Sequence 12, Appl
4	293.8	91.5	375	3	US-09-647-468-13	Sequence 13, Appl
5	287	89.4	1228	2	US-08-401-908-35	Sequence 35, Appl
6	287	89.4	1300	2	US-08-401-908-34	Sequence 34, Appl
7	278.4	86.7	312	2	US-07-789-344A-7	Sequence 7, Appli
8	277.4	86.4	295	2	US-08-401-908-4	Sequence 4, Appli
9	239.4	74.6	366	3	US-09-140-084-22	Sequence 22, Appl
10	239.4	74.6	366	3	US-09-140-084-23	Sequence 23, Appl
11	239.4	74.6	366	3	US-09-724-297-21	Sequence 21, Appl
12	239.4	74.6	366	3	US-09-724-297-22	Sequence 22, Appl
13	239.4	74.6	366	3	US-09-724-108-21	Sequence 21, Appl
14	239.4	74.6	366	3	US-09-724-108-22	Sequence 22, Appl
15	239.4	74.6	366	3	US-09-009-388C-21	Sequence 21, Appl
16	239.4	74.6	366	3	US-09-009-388C-22	Sequence 22, Appl
17	239.4	74.6	724	3	US-09-237-061-1	Sequence 1, Appli
18	236.2	73.6	366	3	US-09-140-084-24	Sequence 24, Appl
19	236.2	73.6	366	3	US-09-724-297-23	Sequence 23, Appl
20	236.2	73.6	366	3	US-09-724-108-23	Sequence 23, Appl
21	236.2	73.6	366	3	US-09-009-388C-23	Sequence 23, Appl
22	231.4	72.1	324	2	US-09-914-695-1	Sequence 1, Appli
23	231.4	72.1	384	2	US-08-379-057-11	Sequence 11, Appl
24	229.8	71.6	324	2	US-08-378-939-31	Sequence 31, Appl
25	229.8	71.6	324	2	US-08-378-939-33	Sequence 33, Appl
26	228.2	71.1	729	2	US-08-230-843-3	Sequence 3, Appli
27	228.2	71.1	729	2	US-08-636-936-3	Sequence 3, Appli
28	228.2	71.1	979	3	US-09-770-916-3	Sequence 3, Appli
29	228.2	71.1	1632	3	US-08-792-824-8	Sequence 8, Appli
30	226.6	70.6	420	9	5219996-18	Patent No. 5219996
31	226.6	70.6	714	3	US-09-472-087-62	Sequence 62, Appl
32	226.6	70.6	754	6	US-07-958-140-1	Sequence 1, Appli
33	226.6	70.6	754	2	PCT-US93-09166-1	Sequence 1, Appli
34	226.6	70.6	1641	3	US-08-792-824-5	Sequence 5, Appli
35	226.6	70.6	1644	2	US-08-792-824-11	Sequence 11, Appl
36	226.6	70.6	1672	2	US-08-792-824-2	Sequence 2, Appli
37	226.6	70.6	4435	2	US-08-792-824-1	Sequence 1, Appli
38	226.6	70.6	5711	3	US-09-897-511A-8	Sequence 8, Appli
39	226.6	70.6	6255	3	US-09-897-511A-13	Sequence 13, Appl
40	225	70.1	381	3	US-09-136-315-3	Sequence 3, Appli
41	225	70.1	381	3	US-09-767-888-3	Sequence 3, Appli
42	225	70.1	819	2	US-08-400-115-3	Sequence 3, Appli
43	225	70.1	927	2	US-07-690-192-1	Sequence 1, Appli
44	223.4	69.6	381	3	US-08-933-985-6	Sequence 6, Appli
45	222.4	69.3	751	6	PCT-US94-07659-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-814-806-1
; Sequence 1, Application US/08814806
; Patent No. 5986065
; GENERAL INFORMATION:
;   APPLICANT: Wong, Hing C.
;   APPLICANT: Jiao, Jin-an
;   APPLICANT: Esperanza, Nieves
;   APPLICANT: Lawrence, Luepschen
;   TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
;   TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
;   NUMBER OF SEQUENCES: 26
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;   STREET: 130 Water Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02109
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/814,806
;   FILING DATE:
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Corless, Peter F
;   REGISTRATION NUMBER: 33,860
;   REFERENCE/DOCKET NUMBER: 46943
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-523-3400
;   TELEFAX: 617-523-6440
;   TELEX:
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 321 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO

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;       ANTI-SENSE: NO
;       FRAGMENT TYPE:
;       ORIGINAL SOURCE:
US-08-814-806-1

Query Match          100.0%;   Score 321;  DB 2;  Length 321;
Best Local Similarity 100.0%;   Pred. No. 1.2e-96;
Matches  321;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy    241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT  300
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Db    241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT  300

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
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Db    301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 2
US-09-293-854-1
; Sequence 1, Application US/09293854
; Patent No. 655319
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
            Jiao, Jin-an
            Esperanza, Nieves
            Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
                    COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES:26
CORRESPONDENCE ADDRESS:
    ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
    STREET: 130 Water Street
    CITY: Boston
    STATE: MA
    COUNTRY: USA
    ZIP: 02109
COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    COMPUTER: IBM Compatible
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/293,854
    FILING DATE: 16-Apr-1999
    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/814,806
    FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
    NAME: Corless, Peter F
    REGISTRATION NUMBER: 33,860
    REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 617-523-3400
    TELEFAX: 617-523-6440
    TELEX: <Unknown>
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;       INFORMATION FOR SEQ ID NO:1:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 321 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
;       FRAGMENT TYPE: <Unknown>
;       ORIGINAL SOURCE:
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-293-854-1

Query Match          100.0%;   Score 321;  DB 3;  Length 321;
Best Local Similarity 100.0%;   Pred. No. 1.2e-96;
Matches  321;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC  60
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Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAACCA  120
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Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCGTGCCACCAACTTGGCAGATCAGCAGCCTCCATCA  180
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Db    121 GGGAAATCTCCTCAGCTCCTGATTTATGCGTGCCACCAACTTGGCAGATCAGCAGCCTCCATCA  180

Qy    181 AGGTTCAGTGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT  240
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Db    181 AGGTTCAGTGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT  240

Qy    241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT  300
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Db    241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT  300

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
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Db    301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 3
US-09-647-468-12
; Sequence 12, Application US/09647468
; Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
    LENGTH: 375
    TYPE: DNA
    ORGANISM: Mus sp.
    FEATURE:
    OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
    OTHER INFORMATION: sequence coding for L chain V region of anti-TF
    OTHER INFORMATION: mouse monoclonal antibody ATR-2
    NAME/KEY: sig_peptide
    LOCATION: (1)..(54)
    NAME/KEY: mat_peptide
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;  LOCATION: (55)..(375)
;  NAME/KEY: CDS
;  LOCATION: (1)..(375)
US-09-647-468-12

Query Match           91.5%;   Score 293.8;  DB 3;  Length 375;
Best Local Similarity 94.7%;   Pred. No. 1.4e-87;
Matches  304;  Conservative   0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC  60
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Db     55 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 114

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||||
Db    115 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 174

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            ||||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||| 
Db    175 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 234

Qy    181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||| 
Db    235 AGGTTCAGTGGCAGTCGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 294

Qy    241 GAAGATTTTGTAAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db    295 GAAGATTTTGTAAGTTATTACTGTCAACAACTTACAGTACTCCGTACACGTTCGGAGGG 354

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
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Db    355 GGGACCAAGCTGGAAATAAAA 375

US-09-647-468-13


RESULT 4
US-09-647-468-13
;  Sequence 13, Application US/09647468
;  Patent No. 6677436
;  GENERAL INFORMATION:
;    APPLICANT:  SATO, KOH
;    APPLICANT:  ADACHI, HIDEKI
;    APPLICANT:  YABUTA, NAOHIRO
;    TITLE OF INVENTION:  HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
;    TITLE OF INVENTION:  PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
;    FILE REFERENCE: 053466/0289
;    CURRENT APPLICATION NUMBER: US/09/647,468
;    CURRENT FILING DATE: 2000-09-29
;    PRIOR APPLICATION NUMBER: PCT/JP99/01768
;    PRIOR FILING DATE: 1999-04-02
;    PRIOR APPLICATION NUMBER: JP 10-91850
;    PRIOR FILING DATE: 1998-04-03
;    NUMBER OF SEQ ID NOS: 183
;    SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;    LENGTH: 375
;    TYPE: DNA
;    ORGANISM: Mus sp.
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
;    OTHER INFORMATION: sequence coding for L chain V region of anti-TF
;    OTHER INFORMATION: mouse monoclonal antibody ATR-3
;    NAME/KEY: sig_peptide
;    LOCATION: (1)..(54)
;    NAME/KEY: mat_peptide
;    LOCATION: (55)..(375)
;    NAME/KEY: CDS
;    LOCATION: (1)..(375)
US-09-647-468-13

Query Match           91.5%;   Score 293.8;  DB 3;  Length 375;
Best Local Similarity 94.7%;   Pred. No. 1.4e-87;
Matches  304;  Conservative   0;  Mismatches   17;  Indels    0;  Gaps    0;
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Db     55 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 114

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db    115 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 174

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            ||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||
Db    175 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 234

Qy    181 AGGTTCAGTGGCAGTCGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    235 AGGTTCAGTGGCAGTCGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 294

Qy    241 GAAGATTTTGTAAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
            ||||||||| |||||||||||||||||||||||| ||||||| ||||| |||||||||||
Db    295 GAAGATTTTGTAAGTTATTACTGTCAACAACTTACAGTACTCCGTACACGTTCGGAGGG 354

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
            |||||||||||||||| |||
Db    355 GGGACCAAGCTGGAAATAAAA 375


RESULT 5
US-08-401-908-35
;  Sequence 35, Application US/08401908
;  Patent No. 5684146
;  GENERAL INFORMATION:
;    APPLICANT:  Yoshinobu OKUNO et al.
;    TITLE OF INVENTION:  A DNA WHICH CODES FOR THE VARIABLE REGION OF
;    TITLE OF INVENTION:  ANTIBODY
;    NUMBER OF SEQUENCES: 36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;      COMPUTER: IBM Compatible
;      OPERATING SYSTEM: MS-DOS
;      SOFTWARE: Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/401,908
;      FILING DATE: March 10, 1995
;      CLASSIFICATION: 536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
; INFORMATION FOR SEQ ID NO: 35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 1228
;      TYPE: nucleic acid
;      STRANDEDNESS: double
;      TOPOLOGY: linear
US-08-401-908-35

Query Match           89.4%;   Score 287;  DB 2;  Length 1228;
Best Local Similarity 93.7%;   Pred. No. 4.4e-85;
Matches  299;  Conservative   0;  Mismatches   20;  Indels    0;  Gaps    0;
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RESULT 6
US-08-401-908-34
; Sequence 34, Application US/08401908
; Patent No. 5684146
; GENERAL INFORMATION:
;   APPLICANT: Yoshinobu OKUNO et al.
;   TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF
;   TITLE OF INVENTION: ANTIBODY
;   NUMBER OF SEQUENCES: 36
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Wenderoth, Lind & Ponack
;   STREET: 805 Fifteenth Street, N.W., #700
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: U.S.A.
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: Wordperfect 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/401,908
;   FILING DATE: March 10, 1995
;   CLASSIFICATION: 536
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Warren M. Cheek, Jr.
;   REGISTRATION NUMBER: 33,367
;   REFERENCE/DOCKET NUMBER:
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-371-8850
;   TELEFAX:
;   TELEX:
; INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1300;
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-08-401-908-34

Query Match   89.4%; Score 287; DB 2; Length 1300;
Best Local Similarity 93.7%; Pred. No. 4.5e-85;
Matches 299; Conservative   0; Mismatches   20; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCGTCTGCATCTCTGGGAGAAAGTGTCACC 60
          |||| || || |||||||||||||||||||||||||||||||||||||||||||||||
Db 517 GACATCGAGCTCACCCAGTCTCCTGCCTCCGTCTGCATCTCTGGGAGAAAGTGTCACC 576

Qy   61 ATCACATGCCTGGCAAGTCAGACATCAGACACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db 577 ATCACATGCCTGGCAAGTCAGACATCAGACACCATTGGTTACATGGTATCAGCAGAAACCA 636

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          ||||||||||||||||||||||||||||||||||| |||||||||||| |||||||||||
Db 637 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAGCTTGGCAGATGGGGTCCCATCA 696

Qy 181 AGGTTCAGTGCAGTGGATCTGGACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
          ||||||||||||||||||||||||||| ||||||||||||||||||| ||||||||
Db 697 AGGTTCAGTGGTAGTGGATCTGGCAACAGCTTTACAGTACTCCGGTTCGGTGGA 756

Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 757 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGGACGTTCGGTGGA 816

Qy 301 GGGACCAAGCTGGAGCTGA 319
          ||||||||||||||||||
Db 817 GGCACCAAGCTGGAGTCGA 835

RESULT 7
US-07-789-344A-7
; Sequence 7, Application US/07789344A
; Patent No. 5318897
; GENERAL INFORMATION:
;   APPLICANT: Sudhir, Paul
;   TITLE OF INVENTION: MONOCLONAL ANTIBODY AND ANTIBODY
;   TITLE OF INVENTION: COMPONENTS ELICITED TO A POLYPEPTIDE ANTIGEN
;   TITLE OF INVENTION: GROUND STATE
;   NUMBER OF SEQUENCES: 13
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Curtis, Morris & Safford
;   ADDRESSEE: c/o Barry Evans
;   STREET: 530 Fifth Avenue
;   CITY: New York
;   STATE: New York
;   COUNTRY: United States of America
;   ZIP: 10036
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/789,344A
;   FILING DATE: 08-NOV-1991
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Evans, Barry
;   REGISTRATION NUMBER: 22,802
;   REFERENCE/DOCKET NUMBER: 370068-3500
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 840-3333
;   TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 312 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-07-789-344A-7

Query Match   86.7%; Score 278.4; DB 2; Length 312;
Best Local Similarity 93.3%; Pred. No. 1.7e-82;
Matches 291; Conservative   0; Mismatches   21; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACGCAGTCTCCCAGTCTGCATCTGTGTCTCCAGGAGAAAGTGTCACC 60
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db 589 GACATCGAGCTCACCCAGTCTCCCAGTCTGCATCTGTGTCTCCAGGAGAAAGTGTCACC 648

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
          ||||||||||||||||||||||| |||||||| ||||||||||||||||||||||||||
Db 649 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 708

Qy 121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db 709 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAGCTTGGCAACCAGCTTGGGGTCCCATCA 768

Qy 181 AGGTTCAGTGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db 769 AGGTTCAGTGGTAGTGGATCTGGCAACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 828

Qy 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db 829 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGGACGTTCGGTGTGGA 888

Qy 301 GGGACCAAGCTGGAGCTGA 319
          ||||||||||||||||||
Db 889 GGCACCAAGCTGGAGTCGA 907

```
Db         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC    60

Qy    61 ATCACATGCCTGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ATCACATGCCTGCAAGTCAGACCATTGATACATGGTTACCATGGTATCAGCAGAAACTA   120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGATATATGCTGCAACCAGCTTGGCAGATGGGGTCCCATCA   180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT   240
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   181 AGGTTCAGTGGTGGTGGATCTGGTCAACATCTTCACACATGTTACAGTTACAGTTACACACA  240

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTCTCCATTCACGTTCG             295
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTGGACGTTCG      295
```

RESULT 8
US-08-401-908-4
; Sequence 4, Application US/08401908
; Patent No. 5684146
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF
; TITLE OF INVENTION: ANTIBODY
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,908
; FILING DATE: March 10, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA to cDNA
US-08-401-908-4

Query Match   86.4%; Score 277.4; DB 2; Length 295;
Best Local Similarity 96.3%; Pred. No. 3.6e-82;
Matches 284; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy     1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC    60
```

RESULT 9
US-09-140-084A
; Sequence 22, Application US/09140084A
; Patent No. 6300065
; GENERAL INFORMATION:
; APPLICANT: Kieke, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: D6061CIP2
; CURRENT APPLICATION NUMBER: US/09/140,084A
; CURRENT FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR products of
; OTHER INFORMATION: wild type scFv-KJ16
US-09-140-084-22

Query Match   74.6%; Score 239.4; DB 3; Length 366;
Best Local Similarity 84.1%; Pred. No. 1.7e-69;
Matches 270; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

```
Qy     1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC    60
          || |||| | ||||| |||   || || |||||||| |||| ||||||||||||||||||
Db     1 GACGTCCTGGTGACCCAAACTCCGCTCTCCTGTCTGCATCTCCGGATGAATCTGTCACC    60

Qy    61 ATCACATGCCTGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA   120
          |||||||||||||||| || ||  | || ||  ||||| |||||||||||||||||||||
Db    61 ATCACATGCCGAGGCCAGGACAGCCAGGACATTGGTACTTCGTTAGTTGGTATCAGCAGAAACCA   120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA   180
          ||||||||||||||||||||| |  |   ||| || |||| ||||||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGTCTATAGTCTATCTTGGCAGATGGGGTCCCATCA       180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT   240
          |||||||||||||||||||||||    |  |||||  || ||  | || || | ||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGGTGTCTATAGTCTTAAGATCAACAGACTACAGGTT   240

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTCTCCATTCACGTTCGGTGCT         300
          |||||| ||| | ||||  || | |||   |||| ||| ||||| ||||| |||
Db   241 GAAGATATTGGAACCTATTACTGTCAGCAGTTTCTCAGTTCTCCGTACACGTTTGGAGCT    300

Qy   301 GGGACCAAGCTGGAGCTGAAA   321
          |||||||||||| |||  ||
Db   301 GGGACCAAGCTGGGAGCTCAA   321
```

RESULT 10
US-09-140-084A
; Sequence 23, Application US/09140084A

; Patent No. 6300065
; GENERAL INFORMATION:
;   APPLICANT: Kieke, et al.
;   TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
;   FILE REFERENCE: D6061CIP2
;   CURRENT APPLICATION NUMBER: US/09/140,084A
;   CURRENT FILING DATE: 1998-08-26
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 366
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PCR products of
;   OTHER INFORMATION: KJ16-mut4
US-09-140-084-23

Query Match   74.6%;   Score 239.4; DB 3; Length 366;
Best Local Similarity 84.1%;   Pred. No. 1.7e-69;
Matches 270; Conservative   0; Mismatches 51; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
            ||||||||||| ||||||| ||| |||||||||||||||||||||| ||| |||||||
Db   1 GACGTCCTGGTGACCCAAACTCCTGCCTCCCTGTCTGCGCATCTCCGATGAATCTGTCACC 60

Qy   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAAACCA 120
            |||||||||||||||||||| |||||| ||| |||||||||||||||||||||||||||
Db   61 ATCACATGCCAGGCAAGCCAGGACATTGGTACTTCGTTAGTTGGTATCAGCAGAAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTATGCTGCCACCAACTGGCAGTGGGGTCCCATCA 180
            |||||||||||||||||||| ||| |||| |||||||| |||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGGTCTATAGTGCAACTATCTTGGCAGATCAGCAGCCTACAGGCT 180

Qy   181 AGGTTCAGTGCAGTGGATCTGGACAAAAATTTCTTTCAAGATACAGTTCTCAACAAGTTTACAGTTCTCAACAAGTTTACAGT 240
            |||||||||||||||||||||||| ||| ||| ||||||||||||||||||||||
Db   181 AGGTTCAGTGCAGTGGATCTGGCAGTAGATCTGGCAGTAGATCTGCCAGATGGGGTCCCATCA 240

Qy   241 GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
            ||||||| || |||| ||||||||||| ||| |||||||||||||||||||||
Db   241 GAAGATATTGGAACCTATTACTGTCTACAGTGTTCTAGTTCTCCGTACACGTTTGGAGCT 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
            || ||||||||||||| |||
Db   301 GGCACCAAGCTGGAGCTCAAA 321

RESULT 11
US-09-724-297-21
; Sequence 21, Application US/09724297
; Patent No. 6423538
; GENERAL INFORMATION:
;   APPLICANT: The Board of Trustees of the University of Illinois
;   APPLICANT: Wittrup, et al.
;   TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
;   FILE REFERENCE: 97-99C
;   CURRENT APPLICATION NUMBER: US/09/724,297
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: US 09/009,388
;   PRIOR FILING DATE: 1998-01-20
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 366
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..(7)
;   OTHER INFORMATION: PCR products of wild type scFv-KJ16
US-09-724-297-21

Query Match   74.6%;   Score 239.4; DB 3; Length 366;

Best Local Similarity 84.1%;   Pred. No. 1.7e-69;
Matches 270; Conservative   0; Mismatches 51; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
            ||||||||||| ||||||| ||| |||||||||||||||||||||| ||| |||||||
Db   1 GACGTCCTGGTGACCCAAACTCCTGCCTCCCTGTCTGCGCATCTCCGATGAATCTGTCACC 60

Qy   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAAACCA 120
            |||||||||||||||||||| |||||| ||| |||||||||||||||||||||||||||
Db   61 ATCACATGCCAGGCAAGCCAGGACATTGGTACTTCGTTAGTTGGTATCAGCAGAAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTATGCTGCCACCAACTGGCAGTGGGGTCCCATCA 180
            |||||||||||||||||||| ||| |||| |||||||| |||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGGTCTATAGTGCAACTATCTTGGCAGATCAGCAGCCTACAGGCT 180

Qy   181 AGGTTCAGTGCAGTGGATCTGGACAAAAATTTCTTTCAAGATACAACAGTATTCTCTTAAGATCAACAGACTACAGGTT 240
            |||||||||||||||||||||||| ||| ||| ||||||||||||||||| || ||||||||||||
Db   181 AGGTTCAGTGCAGTGGATCTGGCAGTAGATCTGTTCCGTACACGTTTCTTCCGTACACGTTTGGAGCT 240

Qy   241 GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
            ||||||| || |||| ||||||||||| ||| |||||||||||||||||||||
Db   241 GAAGATATTGGAACCTATTACTGTCTACAGTGTTCTAGTTCTCCGTACACGTTTGGAGCT 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
            || ||||||||||||| |||
Db   301 GGCACCAAGCTGGAGCTCAAA 321

RESULT 12
US-09-724-297-22
; Sequence 22, Application US/09724297
; Patent No. 6423538
; GENERAL INFORMATION:
;   APPLICANT: The Board of Trustees of the University of Illinois
;   APPLICANT: Wittrup, et al.
;   TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
;   FILE REFERNCE: 97-99C
;   CURRENT APPLICATION NUMBER: US/09/724,297
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: US 09/009,388
;   PRIOR FILING DATE: 1998-01-20
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 366
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..(7)
;   OTHER INFORMATION: PCR products of KJ16-mut4
US-09-724-297-22

Query Match   74.6%;   Score 239.4; DB 3; Length 366;
Best Local Similarity 84.1%;   Pred. No. 1.7e-69;
Matches 270; Conservative   0; Mismatches 51; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
            ||||||||||| ||||||| ||| |||||||||||||||||||||| ||| |||||||
Db   1 GACGTCCTGGTGACCCAAACTCCTGCCTCCCTGTCTGCGCATCTCCGATGAATCTGTCACC 60

Qy   61 ATCACATGCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAAACCA 120
            |||||||||||||||||||| |||||| ||| |||||||||||||||||||||||||||
Db   61 ATCACATGCCAGGCAAGCCAGGACATTGGTACTTCGTTAGTTGGTATCAGCAGAAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTATGCTGCCACCAACTGGCAGTGGGGTCCCATCA 180
            |||||||||||||||||||| ||| |||| |||||||| |||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGGTCTATAGTGCAACTATCTTGGCAGATCAGCAGCCTACAGGCT 180

Qy   181 AGGTTCAGTGCAGTGGATCTGGACAAAAATTTCTTTCAAGATCAACAGTATTCTCTTAAGATCAACACAGGTT 240
            |||||||||||||||||||||||| ||| ||| ||||||||||||||||| | ||||||||||||
Db   181 AGGTTCAGTGCAGTGGATCTGGCAGTAGATCTGGCAGTAGATCTGCCAGATGGGGTCCCATCA 240

Qy   241 GAAGATTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
         |||||| ||| ||| ||||||||| ||||| ||||| |||||| || ||| || |||
Db   241 GAAGATATTGGAACCTATTACTGTCTACAGGTTTCTAGTTCTCCGTACACGTTTGGAGCT 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
         || |||||||||||||||||||
Db   301 GGCACCAAGCTGGAGCTCAAA 321

RESULT 13
US-09-724-108-21
; Sequence 21, Application US/09724108
; Patent No. 6696251
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Illinois
; APPLICANT: Wittrup, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: 97-99D
; CURRENT APPLICATION NUMBER: US/09/724,108
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 366
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: PCR products of wild type scFv-KJ16
US-09-724-108-21

Query Match 74.6%; Score 239.4; DB 3; Length 366;
Best Local Similarity 84.1%; Pred. No. 1.7e-69;
Matches 270; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
         ||| |||| ||||||||||||||||||||||| ||| ||||| |||| ||||||||
Db   1 GACGTCCTGGTGACCCAAACTCCTGCCTCCCTGTCTGCATCTCCGGATGAATCTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
         |||||||||| ||| ||||||| || | | || |||| ||| ||||||||||||||||
Db   61 ATCACATGCCAGGCAAGCCAGGACATTGGTGTCTTAGTTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
         |||||||||||| ||||||| ||| ||| || | | | ||||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGTCTATAGTGCAACATCTCTGGCAGATGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGGACAGACTTCTTCAAGATCAGCAGCCTACAGGCT 240
         ||||||||||||||||||| |||| | || ||||||| ||| |||| ||||||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGGACACACAGATTTCACTCTCTACATCAACAGACTACAGGTT 240

Qy   241 GAAGATTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
         |||||| ||| ||| |||||||| ||||| ||||| ||||| || ||| || |||
Db   241 GAAGATATTGGAACCTATTACTGTCTACAGGTTTCTAGTTCTCCGTACACGTTTGGAGCT 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
         || |||||||||||||||||||
Db   301 GGCACCAAGCTGGAGCTCAAA 321

RESULT 14
US-09-724-108-22
; Sequence 22, Application US/09724108
; Patent No. 6696251
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Illinois
; APPLICANT: Wittrup, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: 97-99D
; CURRENT APPLICATION NUMBER: US/09/724,108
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 366
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: PCR products of KJ16-mut4
US-09-724-108-22

Query Match 74.6%; Score 239.4; DB 3; Length 366;
Best Local Similarity 84.1%; Pred. No. 1.7e-69;
Matches 270; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCTCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
         ||| |||| ||||||||||||||||||||||| ||| ||||| |||| ||||||||
Db   1 GACGTCCTGGTGACCCAAACTCCTGCCTCCCTGTCTGCATCTCCGGATGAATCTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
         |||||||||| ||| ||||||| || | | || |||| ||| ||||||||||||||||
Db   61 ATCACATGCCAGGCAAGCCAGGACATTGGTGTCTTAGTTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
         |||||||||||| ||||||| ||| ||| || | | | ||||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGTCTATAGTGCAACATCTCTGGCAGATGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGGACAGACTTCTTCAAGATCAGCAGCCTACAGGCT 240
         ||||||||||||||||||| |||| | || ||||||| ||| |||| ||||||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGGACACACAGATTTCACTCTCTACATCAACAGACTACAGGTT 240

Qy   241 GAAGATTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
         |||||| ||| ||| |||||||| ||||| ||||| ||||| || ||| || |||
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Qy   301 GGGACCAAGCTGGAGCTGAAA 321
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RESULT 15
US-09-009-388C-21
; Sequence 21, Application US/0900938BC
; Patent No. 6699658
; GENERAL INFORMATION:
; APPLICANT: Wittrup et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCGREGOR & ADLER, LLP
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Office 98
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,388C
; FILING DATE: 20 JAN 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/866,398
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:

```
;       NAME:  Benjamin Aaron Adler, Ph.D.
;       REGISTRATION NUMBER:  35,423
;       REFERENCE/DOCKET NUMBER:  D6061
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE:  (713) 777-2321
;          TELEFAX:   (713) 777-6908
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  366 bp
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double-stranded
;       TOPOLOGY:  linear
;    MOLECULE TYPE:
;       DESCRIPTION:  other nucleic acid
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-09-009-388C-21
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Best Local Similarity   84.1%;   Pred. No. 1.7e-69;
Matches  270;  Conservative   0;  Mismatches  51;  Indels    0;  Gaps    0;

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Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
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Job time : 169 secs

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              GenCore version 5.1.7
       Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:   April 18, 2006, 18:27:07 ; Search time 574 Seconds
                                    (without alignments)
          4624.513 Million cell updates/sec

Title:         US-10-764-140-1
Perfect score: 321
Sequence:      1 gacattcagatgaccagtc........ggaccaagctggagctgaaa 321

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:    19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA_Main:*
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    8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
    9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
   10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	321	100.0	321	3	US-09-293-854-1	Sequence 1, Appli
2	321	100.0	321	3	US-09-990-586-1	Sequence 1, Appli
3	321	100.0	321	5	US-10-293-417-1	Sequence 1, Appli
4	321	100.0	321	6	US-10-310-113-1	Sequence 1, Appli
5	321	100.0	321	6	US-10-230-880-1	Sequence 1, Appli
6	321	100.0	321	8	US-10-764-140-1	Sequence 1, Appli
7	321	100.0	321	9	US-10-618-338-1	Sequence 1, Appli
8	293.8	91.5	375	7	US-10-462-062-12	Sequence 12, Appl
9	292.2	91.1	375	7	US-10-462-062-13	Sequence 13, Appl
10	239.4	74.6	321	10	US-11-036-098-15	Sequence 15, Appl
11	239.4	74.6	366	7	US-10-738-454-21	Sequence 21, Appl
12	239.4	74.6	366	7	US-10-738-454-22	Sequence 22, Appl
13	239.4	74.6	724	3	US-09-237-061-1	Sequence 1, Appli
14	236.2	73.6	366	7	US-10-738-454-23	Sequence 23, Appl
15	236.2	73.6	1637	10	US-11-036-098-17	Sequence 17, Appl
16	231.4	72.1	324	7	US-10-762-629-1	Sequence 1, Appli
17	229.8	71.6	702	9	US-10-500-696-3	Sequence 3, Appli
18	228.2	71.1	768	9	US-10-239-656-56	Sequence 56, Appl
19	228.2	71.1	882	9	US-10-496-059-5	Sequence 5, Appli
20	228.2	71.1	979	3	US-09-770-916-3	Sequence 3, Appli
21	228.2	71.1	979	3	US-10-496-059-3	Sequence 3, Appli
22	228.2	71.1	1509	7	US-10-239-656-74	Sequence 74, Appl
23	226.6	70.6	321	5	US-10-073-644C-3	Sequence 3, Appli
24	226.6	70.6	321	7	US-10-239-656-7	Sequence 7, Appli
25	226.6	70.6	387	3	US-09-791-551-51	Sequence 51, Appl
26	226.6	70.6	714	5	US-10-153-382-18	Sequence 18, Appl
27	226.6	70.6	714	8	US-10-612-497-62	Sequence 62, Appl
28	226.6	70.6	714	8	US-10-776-649-62	Sequence 62, Appl
29	226.6	70.6	714	10	US-11-085-368-18	Sequence 18, Appl
30	226.6	70.6	5711	3	US-09-897-006-8	Sequence 8, Appli
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33	226.6	70.6	5711	8	US-10-759-315-8	Sequence 8, Appli
34	226.6	70.6	5711	9	US-10-947-881-8	Sequence 8, Appli
35	226.6	70.6	5711	10	US-11-018-895-8	Sequence 8, Appli
36	226.6	70.6	5711	10	US-11-036-557-8	Sequence 8, Appli
37	226.6	70.6	6255	3	US-09-897-006-13	Sequence 13, Appl
38	226.6	70.6	6255	3	US-09-897-511A-13	Sequence 13, Appl
39	226.6	70.6	6255	6	US-10-397-079-13	Sequence 13, Appl
40	226.6	70.6	6255	8	US-10-759-315-13	Sequence 13, Appl
41	226.6	70.6	6255	9	US-10-947-881-13	Sequence 13, Appl
42	226.6	70.6	6255	10	US-11-018-895-13	Sequence 13, Appl
43	226.6	70.6	6255	10	US-11-036-557-13	Sequence 13, Appl
44	225	70.1	381	3	US-09-767-888-3	Sequence 3, Appli
45	225	70.1	381	6	US-10-289-181-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-09-293-854-1
; Sequence 1, Application US/09293854
; Patent No. US2002016857A1
; GENERAL INFORMATION:
;  APPLICANT: Wong, Hing C.
;             Jiao, Jin-an
;             Esperanza, Nieves
;             Lawrence, Luepschen
;  TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
;                      COAGULATION AND METHODS OF USE THEREOF
;  NUMBER OF SEQUENCES: 26
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;   STREET: 130 Water Street
;   CITY: Boston
;   STATE: MA
;   COUNTRY: USA
;   ZIP: 02109
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 1.5
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/293,854
;   FILING DATE: 16-Apr-1999
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/814,806
;   FILING DATE: <Unknown>
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Corless, Peter F
;   REGISTRATION NUMBER: 33,860
;   REFERENCE/DOCKET NUMBER: 46943
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 617-523-3400
;   TELEFAX: 617-523-6440
;   TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 321 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
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;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: <Unknown>
;     ORIGINAL SOURCE:
;     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-293-854-1

Query Match             100.0%;  Score 321; DB 3;  Length 321;
Best Local Similarity   100.0%;  Pred. No. 7e-94;
Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy    181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
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Qy    241 GAAGATTTGTAAATTATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db    241 GAAGATTTGTAAATTATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
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RESULT 2
US-09-990-586-1
; Sequence 1, Application US/09990586
; Publication No. US2003010968OA1
; GENERAL INFORMATION:
;     APPLICANT: JIAO, JIN-AN
;     APPLICANT: WONG, HING C.
;     TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
;     TITLE OF INVENTION: OF USE THEREOF
;     FILE REFERENCE: 71758/46943-CIP2
;     CURRENT APPLICATION NUMBER: US/09/990,586
;     CURRENT FILING DATE: 2001-11-21
;     PRIOR APPLICATION NUMBER: 09/293,854
;     PRIOR FILING DATE: 1999-04-16
;     NUMBER OF SEQ ID NOS: 102
;     SOFTWARE: PatentIn Ver. 2.1
;     SEQ ID NO 1
;     LENGTH: 321
;     TYPE: DNA
;     ORGANISM: Homo sapiens
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (1)..(321)
US-09-990-586-1

Query Match             100.0%;  Score 321; DB 3;  Length 321;
Best Local Similarity   100.0%;  Pred. No. 7e-94;
Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    241 GAAGATTTGTAAATTATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db    241 GAAGATTTGTAAATTATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
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Db    301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 3
US-10-293-417-1
; Sequence 1, Application US/10293417
; Publication No. US2003008263AA1
; GENERAL INFORMATION:
;     APPLICANT: Wong, Hing C.
;                Jiao, Jin-an
;                Esperanza, Nieves
;                Lawrence, Luepschen
;     TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
;                         COAGULATION AND METHODS OF USE THEREOF
;     NUMBER OF SEQUENCES: 26
;     CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
;         STREET: 130 Water Street
;         CITY: Boston
;         STATE: MA
;         COUNTRY: USA
;         ZIP: 02109
;     COMPUTER READABLE FORM:
;         MEDIUM TYPE: Diskette
;         COMPUTER: IBM Compatible
;         OPERATING SYSTEM: DOS
;         SOFTWARE: FastSEQ Version 1.5
;     CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/10/293,417
;         FILING DATE: 12-No. US2003008263AA1-2002
;         CLASSIFICATION: <Unknown>
;     PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US/09/293,854
;         FILING DATE: 16-Apr-1999
;         APPLICATION NUMBER: 08/814,806
;         FILING DATE: <Unknown>
;     ATTORNEY/AGENT INFORMATION:
;         NAME: Corless, Peter F
;         REGISTRATION NUMBER: 33,860
;         REFERENCE/DOCKET NUMBER: 46943
;     TELECOMMUNICATION INFORMATION:
;         TELEPHONE: 617-523-3400
;         TELEFAX: 617-523-6440
;         TELEX: <Unknown>
;     INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 321 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: <Unknown>
;     ORIGINAL SOURCE:
;     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-293-417-1

Query Match             100.0%;  Score 321; DB 5;  Length 321;
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RESULT 4
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; Sequence 1, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
;  APPLICANT: JIAO, JIN-AN
;  APPLICANT: WONG, HING C.
;  APPLICANT: NIEVES, ESPERANZA LILIANA
;  APPLICANT: MOSQUERA, LUIS A.
;  TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
;  TITLE OF INVENTION: THROMBOSES
;  FILE REFERENCE: 58122(71758)
;  CURRENT APPLICATION NUMBER: US/10/310,113
;  CURRENT FILING DATE: 2002-12-04
;  PRIOR APPLICATION NUMBER: 09/990,586
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/343,306
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: 09/293,854
;  PRIOR FILING DATE: 1999-04-16
;  PRIOR APPLICATION NUMBER: 08/814,806
;  PRIOR FILING DATE: 1997-03-10
;  NUMBER OF SEQ ID NOS: 169
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;  LENGTH: 321
;  TYPE: DNA
;  ORGANISM: Murine sp.
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(321)
US-10-310-113-1

Query Match    100.0%;  Score 321;  DB 6;  Length 321;
Best Local Similarity  100.0%; Pred. No. 7e-94;
Matches  321; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

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Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACACGGTTAGCATGGTATCAGCAGAAACCA 120
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Qy  241 GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db  241 GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
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Db  301 GGGACCAAGCTGGAGCTGAAA 321


RESULT 5
US-10-230-880-1
; Sequence 1, Application US/1023080
; Publication No. US2003019070SA1
; GENERAL INFORMATION:
;  APPLICANT: WONG, HING C.
;  APPLICANT: STINSON, JEFFREY L.
;  APPLICANT: MOSQUERA, LUIS A.
;  TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
;  FILE REFERENCE: 7175B/58066
;  CURRENT APPLICATION NUMBER: US/10/230,880
;  CURRENT FILING DATE: 2002-12-23
;  PRIOR APPLICATION NUMBER: 09/990,586
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/343,306
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: 09/293,854
;  PRIOR FILING DATE: 1999-04-16
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;  LENGTH: 321
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(321)
US-10-230-880-1

Query Match    100.0%;  Score 321;  DB 6;  Length 321;
Best Local Similarity  100.0%; Pred. No. 7e-94;
Matches  321; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy  181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
        |||||||||||||||||||||
Db  301 GGGACCAAGCTGGAGCTGAAA 321
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RESULT 6
US-10-764-140-1
; Sequence 1, Application US/10764140
; Publication No. US20040229282A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: JIAO, JIN-AN
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: 59918 (71758)
; CURRENT APPLICATION NUMBER: US/10/764,140
; CURRENT FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 10/293,417
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 2002-03-10
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 3.2
;
; SEQ ID NO 1
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-140-1

Query Match   100.0%; Score 321; DB 8; Length 321;
Best Local Similarity 100.0%; Pred. No. 7e-94;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
          |||||||||||||||||||||
Db   301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 7
US-10-618-338-1
; Sequence 1, Application US/10618338
; Publication No. US20050089929A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
;   Jiao, Jin-an
;   Esperanza, Nieves
;   Lawrence, Luepschen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
;   COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston

; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/618,338
; FILING DATE: 11-Jul-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,854
; FILING DATE: 16-Apr-1999
; APPLICATION NUMBER: 08/814,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 46943
; TELECOMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-618-338-1

Query Match   100.0%; Score 321; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 7e-94;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAACCA 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
          |||||||||||||||||||||
Db   301 GGGACCAAGCTGGAGCTGAAA 321

RESULT 8
US-10-462-062-12
; Sequence 12, Application US/10462062
; Publication No. US2004004187A1
; GENERAL INFORMATION:

APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 375
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence
OTHER INFORMATION: coding for L chain V region of anti-TF mouse monoclonal
OTHER INFORMATION: antibody ATR-2
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(375)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)..(54)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (55)..(375)
US-10-462-062-12

Query Match   91.5%; Score 293.8; DB 7; Length 375;
Best Local Similarity 94.7%; Pred. No. 5.5e-85;
Matches 304; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   55 GACATTCAGATGACCCAGTCTCCTGCCTCCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 114

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
        |||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||||
Db  115 ATCACATGCCTGGCAAGTCAGACCATTGGTACATGGTTAGCCTGGTATCAGCAGAAACCA 174

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCACCAAACTTGGCAGATGGGTCCCCATCA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  175 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCACCAAACTTGGCAGATGGGTCCCCATCA 234

Qy  181 AGGTTCAGTGGCAGTGGATCTGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  235 AGGTTCAGTGGCAGTGGATCTGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 294

Qy  241 GAAGATTTTGTAAAATTATTACTGTCAACAAGTTTACAGTTTCCATTCAGTTTCCTACAGGCT 300
        |||||||||||  || ||||||||||||||  ||||||  |||  ||  |||||||||||||
Db  295 GAAGATTTTGTAAGTTATTATTACTGTCAACAACTTTACAGTACTCCGTACACGTTCGGTGCT 354

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
        ||||||||||||||    |||
Db  355 GGGACCAAGCTGGAAATAAAA 375
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PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 375
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence
OTHER INFORMATION: coding for L chain V region of anti-TF mouse monoclonal
OTHER INFORMATION: antibody ATR-3
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(375)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)..(54)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (55)..(375)
US-10-462-062-13

Query Match   91.0%; Score 292.2; DB 7; Length 375;
Best Local Similarity 94.4%; Pred. No. 1.8e-84;
Matches 303; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   55 GACATTCAGATGACCCAGTCTCCTGCCTCCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 114

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 174
        |||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||||
Db  115 ATCACATGCCTGGCAAGTCAGACCATTGGTACATGGTTAGCCTGGTATCAGCAGAAACCA 174

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCACCAAACTTGGCAGATGGGTCCCCATCA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  175 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCACCAAACTTGGCAGATGGGTCCCCATCA 234

Qy  181 AGGTTCAGTGGCAGTGGATCTGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  235 AGGTTCAGTGGCAGTGGATCTGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 294

Qy  241 GAAGATTTTGTAAAATTATTACTGTCAACAAGTTTACAGTTTCCATTCAGTTCCTACAGGCT 300
        |||||||||||  || |||| |||||||||  ||||||  |||  ||  |||||||||||||
Db  295 GAAGATTTTGTAAGTTATTATTACTGTCAACAACTTTACAGTACTCCGTACACGTTCGGAGGG 354

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
        ||||||||||||||    |||
Db  355 GGGACCAAGCTGGAAATAAAA 375
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RESULT 9
US-10-462-062-13
; Sequence 13, Application US/10462062
; Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16

RESULT 10
US-11-036-098-15
; Sequence 15, Application US/11036098
; Publication No. US2005016377OA1
GENERAL INFORMATION:
APPLICANT: Connex GmbH
TITLE OF INVENTION: Immunological reagent specifically interacting with the
TITLE OF INVENTION: extracellular domain of the human zeta chain
FILE REFERENCE: C1368PCT
CURRENT APPLICATION NUMBER: US/11/036,098
CURRENT FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US/09/743,482
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: EP 98 11 2867.1
PRIOR FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 321

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;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(321)
US-11-036-098-15

Query Match      74.6%;    Score 239.4;  DB 10;  Length 321;
Best Local Similarity  84.1%;   Pred. No. 2.7e-67;
Matches  270;  Conservative  0;  Mismatches  51;  Indels  0;  Gaps  0;

Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60
         ||||||||  ||||||  ||||||  ||||| |||||| |||  || ||||   ||||||
Db    1 GACATCCAGATGACACAGTCTCCGTCTCCGTCTGCGTCTCCGGAAGAAAATTGTCACG   60

Qy   61 ATCACATGCCTGGCAGTCAGACCATTGAACATTGATACATGGTTAGCATGGTATCAGCAGAAACCA  120
         ||||||||  ||||| |||  |||| ||||| |||||| ||  || |||||| |||||||||||||
Db   61 ATCACATGCCAGGCAGCCAAGCAGCATTGGTAATTGGTTAGCATTGGTTAGCATGTATCAGCAGAAACCA  120

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
         ||||||||||||  ||||||| |||||| |||||||||||| |||||| ||| ||||||
Db  121 GGGAAATCTCCTCAGCTCCTGGTCTATAGTGCAACCAGCTTGGCAGCGGGATCCCATCA  180

Qy  181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTTCTTTCAAGATCAGCAGCCTACAGGCT  240
         |||||||||||||| ||||||  |||||||||| |||||||||||||||| ||||||||
Db  181 AGGTTCAGTGGCGGCAGTAGATCTGGTACACAGACTATTCTCTTAAGATCAGCAGACTACAGGTT  240

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT  300
         ||||||||  ||  || |||||||  || ||| |||  ||| ||| |||||||||||| ||
Db  241 GAAGATACTGGAATCTATTACTGTCTACAGCGTTATAGTAATCCCAACACGTTTGGAGCT  300

Qy  301 GGGACCAAGCTGGAGCTGAAA  321
         ||||||||||||||||||||
Db  301 GGGACCAAGCTGGAGCTGAAA  321


RESULT 11
US-10-738-454-21
; Sequence 21, Application US/10738454
; Publication No. US20040146976A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Illinois
; APPLICANT: Wittrup, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: 97-99E
; CURRENT APPLICATION NUMBER: US/10/738,454
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 09/724,108
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: US 08/866,398
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/018,741
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 366
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..(7)
; OTHER INFORMATION: PCR products of wild type scFv-KJ16
US-10-738-454-21

Query Match      74.6%;    Score 239.4;  DB 7;  Length 366;
Best Local Similarity  84.1%;   Pred. No. 2.9e-67;
Matches  270;  Conservative  0;  Mismatches  51;  Indels  0;  Gaps  0;

Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60
```

```
Db    1 GACGTCCTGGTGACCCAAACTCCTGCCTCCCTGTCTGCATCTCCGGATGAATCTGTCACC   60

Qy   61 ATCACATGCCTGGCAGTCAGACCATTGAACATTGATACATGGTTAGCATGGTATCAGCAGAAACCA  120
         ||||||||          ||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACATGCCAGGCAGCCAAGCAGCATTGGTACTTCGTTAGCATGGTATCAGCAGAAACCA  120

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
         ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  121 GGGAAATCTCCTCAGCTCCTGGTCTATAGTGCAACTATCTTGGCAGATGGGGTCCCATCA  180

Qy  181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTTCTTTCAAGATCAGCAGCCTACAGGCT  240
         |||||||||||||| ||||||  ||||||||||  |||||||||||||| ||||||||
Db  181 AGGTTCAGTGGCGGCAGTAGATCTGGTACACAGACTATTCTCTTAAGATCAGCAGACTACAGGTT  240

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT  300
         |||||||||||||  ||||||||||  ||||||| |||||| ||  |||||||||||| ||
Db  241 GAAGATATTGGAACCTATTACTGTCTACAGCGTTTCTCAGTCTCCGTACACGTTTGGAGCT  300

Qy  301 GGGACCAAGCTGGAGCTGAAA  321
         ||||||||||||||||||||
Db  301 GGCACCAAGCTGGAGCTCAAA  321


RESULT 12
US-10-738-454-22
; Sequence 22, Application US/10738454
; Publication No. US20040146976A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Illinois
; APPLICANT: Wittrup, et al.
; TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
; FILE REFERENCE: 97-99E
; CURRENT APPLICATION NUMBER: US/10/738,454
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 09/724,108
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: US 08/866,398
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/018,741
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 366
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..(7)
; OTHER INFORMATION: PCR products of KJ16-mut4
US-10-738-454-22

Query Match      74.6%;    Score 239.4;  DB 7;  Length 366;
Best Local Similarity  84.1%;   Pred. No. 2.9e-67;
Matches  270;  Conservative  0;  Mismatches  51;  Indels  0;  Gaps  0;

Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60
         ||||| ||||||||| ||||||||||||||||||||||||||||||||||||| ||||||
Db    1 GACGTCCTGGTGACCCAAACTCCTGCCTCCCTGTCTGCATCTCCGGATGAATCTGTCACC   60

Qy   61 ATCACATGCCTGGCAGTCAGACCATTGAACATTGATACATGGTTAGCATGGTATCAGCAGAAACCA  120
         ||||||||                 ||||||||||||||||||||||||||||||||||||||||
Db   61 ATCACATGCCAGGCAGCCAAGCAGCATTGGTACTTCGTTAGCATGGTATCAGCAGAAACCA  120

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
         |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  121 GGGAAATCTCCTCAGCTCCTGGTCTATAGTGCAACTATCTTGGCAGATGGGGTCCCATCA  180

Qy  181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTTCTTTCAAGATCAGCAGCCTACAGGCT  240
         |||||||||||||| ||||||  ||||||||||  |||||||||||||| ||||||||
Db  181 AGGTTCAGTGGCGGCAGTAGATCTGGTACACAGACTATTCTCTTAAGATCAGCAGACTACAGGTT  240
```

```
Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
            |||||||||||||||||||||||||||| ||||||  |||||||||||||| ||| |||
Db  241 GAAGATATTGGAACCTATTACTGTCTACAGGTTTCTACAGGTTTCGTTCTCCGTACACGTTTGGAGCT 300

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
            || ||||||||||||||| |||
Db  301 GGCACCAAGCTGGAGCTCAAA 321
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RESULT 13
US-09-237-061-1
; Sequence 1, Application US/09237061
; Patent No. US20020081624A1
; GENERAL INFORMATION:
;   APPLICANT: DuPont Pharmaceuticals Company
;   TITLE OF INVENTION: Detection of Patients at Risk for Developing Integrin
;   TITLE OF INVENTION: Antagonist/Agonist Mediated Disease States
;   FILE REFERENCE: DM-6956
;   CURRENT APPLICATION NUMBER: US/09/237,061
;   CURRENT FILING DATE: 1999-01-26
;   PRIOR APPLICATION NUMBER: 60/072,733
;   PRIOR FILING DATE: 1998-01-27
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
;   LENGTH: 724
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Light Chain of
;   OTHER INFORMATION: rJK094
US-09-237-061-1

Query Match   74.6%; Score 239.4; DB 3; Length 724;
Best Local Similarity   84.1%; Pred. No. 3.8e-67;
Matches 270; Conservative   0; Mismatches 51; Indels   0; Gaps   0;

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Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db   74 GACATCCAGATGACTCAGTCTCCAGCCTCCGTGTCTGCATCTGTGGGAGAAACTGTCACC 133

Qy   61 ATCACATGCCTGGCAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Db  134 ATCACATGTCGAGCAAGTGAGATTATTTACACTTATTTAGCATGGTATCAGCAGAAACAG 193

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          ||||||||||||||||||||||||||| |||| ||||||||||||| ||||| |||||||
Db  194 GGGAAATCTCCTCAGCTCCTGATTTATGCTGTCATAATGCAAAAACCTTAGCAGAAGGTGTGCCATCA 253

Qy  181 AGGTTCAGTGGCAGTGGATCTGGGACACAAAATTTTCTTCAAGATCAGCAGGCT 240
          ||||||||||| ||||||||||||| ||||  |||||| ||||| ||||||| ||
Db  254 AGGTTCAGTGGCAGTGGATCAGGGACATCAACAGCCTGCAGCCT 313

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db  314 GAAGATTTTGGGAATTATTATTACTGTCAACATCATTATGGTACTCCGCTCACGTTCGGTGCT 373

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
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Db  374 GGGACCAAGCTGGAGCTGAAA 394
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RESULT 14
US-10-738-454-23
; Sequence 23, Application US/10738454
; Publication No. US2004014697 6A1
; GENERAL INFORMATION:
;   APPLICANT: The Board of Trustees of the University of Illinois
;   APPLICANT: Wittrup, et al.
;   TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
;   FILE REFERENCE: 97-99E
;   CURRENT APPLICATION NUMBER: US/10/738,454

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;   CURRENT FILING DATE: 2003-12-16
;   PRIOR APPLICATION NUMBER: US 09/724,108
;   PRIOR FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: US 09/009,388
;   PRIOR FILING DATE: 1998-01-20
;   PRIOR APPLICATION NUMBER: US 08/866,398
;   PRIOR FILING DATE: 1997-05-30
;   PRIOR APPLICATION NUMBER: US 60/018,741
;   PRIOR FILING DATE: 1996-05-31
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 23
;   LENGTH: 366
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..(7)
;   OTHER INFORMATION: PCR products of KJ16-mut7
US-10-738-454-23

Query Match   73.6%; Score 236.2; DB 7; Length 366;
Best Local Similarity   83.5%; Pred. No. 3.2e-66;
Matches 268; Conservative   0; Mismatches 53; Indels   0; Gaps   0;

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Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db    1 GACGTCCTGGTGACCCAAACTCCGCTCCCTGTCTGCATCTCCGGATGAATCTGTCACC 60

Qy   61 ATCACATGCCTGGCAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
          ||||||||||| |  ||||||||||| |||||||||| |||||| ||||||||||||||||
Db   61 ATCACATGCCAGGCACCGCCAGGACATTGGTACTTCGTTAGTTGGTATCAGCAGAAACCA 120

Qy  121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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Db  121 GGGAAATCTCCTCAGCTCCTGTCTATAGTGCAACTATCTTGGCAGATGGGGTCCCATCA 180

Qy  181 AGGTTCAGTGGCAGTGGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Db  181 AGGTTCAGTGGCAGTGGATCTGGGACATCAACAGTATTCTCTTAAGATCAACAGACTACAGGTT 240

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db  241 GAAGATATTGGAACCTATTACTGTCTACAGGTTTCTACAGGTTTCCCGTACACGTTTGGAGCT 300

Qy  301 GGGACCAAGCTGGAGCTGAAA 321
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Db  301 GGCACCAAGCTGGAGCTCAAA 321
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RESULT 15
US-11-036-098-17
; Sequence 17, Application US/11036098
; Publication No. US2005163770A1
; GENERAL INFORMATION:
;   APPLICANT: Connex GmbH
;   TITLE OF INVENTION: Immunological reagent specifically interacting with the
;   TITLE OF INVENTION: extracellular domain of the human zeta chain
;   FILE REFERENCE: C1368PCT
;   CURRENT APPLICATION NUMBER: US/11/036,098
;   CURRENT FILING DATE: 2005-01-18
;   PRIOR APPLICATION NUMBER: US/09/743,482
;   PRIOR FILING DATE: 2001-02-28
;   PRIOR APPLICATION NUMBER: EP 98 11 2867.1
;   PRIOR FILING DATE: 1998-07-10
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 1637
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic

</div>

; OTHER INFORMATION: construct of DNA encoding bispecific single chain
; OTHER INFORMATION: antibody comprising anti-zeta-chain/anti-EpCAM
; OTHER INFORMATION: domains.
US-11-036-098-17

Query Match   73.6%;   Score 236.2; DB 10; Length 1637;
Best Local Similarity 83.5%;   Pred. No. 5.9e-66;
Matches 268; Conservative   0; Mismatches 53; Indels 0; Gaps 0;

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Qy    1 GACATTCAGATGACCCAGTCTCCTGCCTCCAGTCTGCATCTCTGGGAGAAAGTGTCACC  60
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Db   67 GATATCCAGATGACACAGTCTCCTGCTTCCCTGTCTGCGTCCCGGAAGAAATTGTCACG  126

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA  120
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Db  127 ATCACATGCCAGGCAGGCCAGGACACATTGGTAATTGGTTAGCATGGTATCAGCAGAAACCA  186

Qy  121 GGGAAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
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Db  187 GGGAAAATCTCCTCAACTCCTGATCTATAGTGCAACCAGCTTGGCAGACGGGATCCCATCA  246

Qy  181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT  240
        |||||||| ||| ||||| |||| ||||  ||  |   ||||||||||||||  ||||||| |
Db  247 AGGTTCAGCGGCGGTAGATCTGGTACACAGTATTCTCTTAAGATCAGCAGACTACAGGTT  306

Qy  241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT  300
        ||| |||| || ||| |||  ||||||||||| |||  |||||| || ||||| |||||| |
Db  307 GAAGATACTGGAATCTATTACTGTCTACAGCGTTATAGTAATCCCAACACGTTTGGAGCT  366

Qy  301 GGGACCAAGCTGGAGCTGAAA  321
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Db  367 GGGACCAAGCTGGAGCTGAAA  387
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Search completed: April 18, 2006, 22:26:16
Job time : 575 secs

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                    GenCore version 5.1.7
           Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:      April 18, 2006, 18:31:21 ; Search time 1340 Seconds
                                  (without alignments)
                                  964.876 Million cell updates/sec

Title:      US-10-764-140-1
Perfect score: 321
Sequence:   1 gacattcagatgacccagtc........ggaccaagctgagctgaaa 321

Scoring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0

Searched:   9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters:     18552198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries
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        13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
        14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
        15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	321	100.0	321	11	US-11-122-622-1	Sequence 1, Appli
2	321	100.0	321	14	US-11-087-528-1	Sequence 1, Appli
3	240.2	74.8	411	14	US-11-136-527-190	Sequence 190, App
4	240.2	74.8	411	14	US-11-136-527-4286	Sequence 4286, Ap
5	226.6	70.6	714	14	US-11-128-900-62	Sequence 62, Appl
c 6	226.6	70.6	13281	9	US-10-893-483-188	Sequence 188, App
7	224.6	70.0	322	12	US-11-144-248-54	Sequence 54, Appl
8	224.6	70.0	322	14	US-11-144-222-54	Sequence 54, Appl
9	224.6	70.0	322	14	US-11-182-343-54	Sequence 54, Appl
10	221.8	69.1	708	14	US-11-086-289-7	Sequence 7, Appli
11	221.8	69.1	13281	9	US-10-893-483-188	Sequence 188, App
12	220.2	68.6	324	11	US-11-199-739-173	Sequence 173, App
13	220.2	68.6	324	14	US-11-049-536-173	Sequence 173, App
14	218.6	68.1	322	7	US-10-956-008-75	Sequence 75, Appl
15	218.6	68.1	324	11	US-11-199-739-241	Sequence 241, App
16	218.6	68.1	324	14	US-11-049-536-241	Sequence 241, App
17	218	67.9	326	12	US-11-144-248-53	Sequence 53, Appl
18	218	67.9	326	14	US-11-144-222-53	Sequence 53, Appl
19	218	67.9	218	14	US-11-182-343-53	Sequence 53, Appl
20	217	67.6	12233	9	US-10-893-483-187	Sequence 187, App
c 21	217	67.6	12233	9	US-10-893-483-187	Sequence 187, App
22	215.4	67.1	315	14	US-11-155-775-51	Sequence 51, Appl
23	215.4	67.1	321	14	US-11-084-554-5	Sequence 5, Appli
24	215.4	67.1	321	14	US-11-136-250-5	Sequence 5, Appli
25	215.4	67.1	324	11	US-11-199-739-453	Sequence 453, App
26	215.4	67.1	324	11	US-11-199-739-597	Sequence 597, App
27	215.4	67.1	324	14	US-11-049-536-453	Sequence 453, App
28	215.4	67.1	324	14	US-11-049-536-597	Sequence 597, App
29	215.4	67.1	357	9	US-10-993-543-121	Sequence 121, App
30	215.4	67.1	1721	9	US-10-998-207-27	Sequence 27, Appl
31	213.8	66.6	315	14	US-11-155-775-55	Sequence 55, Appl
32	213.8	66.6	321	14	US-11-051-453-37	Sequence 37, Appl
33	213.8	66.6	322	12	US-11-144-248-13	Sequence 13, Appl
34	213.8	66.6	322	14	US-11-144-222-13	Sequence 13, Appl
35	213.8	66.6	322	14	US-11-182-343-13	Sequence 13, Appl
36	213.8	66.6	324	11	US-11-199-739-481	Sequence 481, App
37	213.8	66.6	324	14	US-11-049-536-481	Sequence 481, App
38	213.8	66.6	388	14	US-11-009-840A-206	Sequence 206, App
39	213.8	66.6	388	14	US-11-009-873A-206	Sequence 206, App
40	213.8	66.6	388	14	US-11-009-769A-206	Sequence 206, App
41	213.8	66.6	708	14	US-11-086-289-3	Sequence 3, Appli
42	213.8	66.6	708	14	US-11-086-289-19	Sequence 19, Appl
43	212.2	66.1	308	11	US-11-199-739-21	Sequence 21, Appl
44	212.2	66.1	308	14	US-11-049-536-21	Sequence 21, Appl
45	212.2	66.1	321	8	US-10-850-635-17	Sequence 17, Appl

ALIGNMENTS

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RESULT 1
US-11-122-622-1
; Sequence 1, Application US/11122622
; Publication No. US20060039901A1
; GENERAL INFORMATION:
;  APPLICANT: JIAO, JIN-AN
;  APPLICANT: WONG, HING C.
;  TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
;  TITLE OF INVENTION:  OF USE THEREOF
;  FILE REFERENCE: 71758/46943-CIP2
;  CURRENT APPLICATION NUMBER: US/11/122,622
;  CURRENT FILING DATE: 2005-05-05
;  PRIOR APPLICATION NUMBER: US/09/990,586
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 09/293,854
;  PRIOR FILING DATE: 1999-04-16
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
;  LENGTH: 321
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)..(321)
US-11-122-622-1

Query Match             100.0%;  Score 321;  DB 11;  Length 321;
Best Local Similarity   100.0%;  Pred. No. 2.4e-92;
Matches  321;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Db      1 GACATTCAGATGACCCAGTCTCCTGCCTCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCGAGATGGGTCCCATCA 180
Qy   181 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Db   181 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Db   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
Qy   301 GGGACCAAGCTGGAGCTGAAA 321
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Db   301 GGGACCAAGCTGGAGCTGAAA 321
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RESULT 2
US-11-087-528-1
; Sequence 1, Application US/11087528
; Publication No. US20050271664A1
; GENERAL INFORMATION:
;   APPLICANT: JIAO, JIN-AN
;   APPLICANT: WONG, HING C.
;   APPLICANT: WEN, JING HAI
;   TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
;   TITLE OF INVENTION: OF USE THEREOF
;   FILE REFERENCE: TNA-005.06
;   CURRENT APPLICATION NUMBER: US/11/087,528
;   CURRENT FILING DATE: 2005-03-22
;   PRIOR APPLICATION NUMBER: 10/293,417
;   PRIOR FILING DATE: 2002-11-12
;   PRIOR APPLICATION NUMBER: 09/293,854
;   PRIOR FILING DATE: 1999-04-16
;   PRIOR APPLICATION NUMBER: 08/814,806
;   PRIOR FILING DATE: 1997-03-10
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(321)
US-11-087-528-1

Query Match   100.0%; Score 321; DB 14; Length 321;
Best Local Similarity 100.0%; Pred. No. 2.4e-92;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCCATCTCTGGGAGAAAGTGTCACC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCCATCTCTGGGAGAAAGTGTCACC 60
Qy    61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCGAGATGGGTCCCATCA 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCGAGATGGGTCCCATCA 180
Qy   181 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Db   181 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
Qy   301 GGGACCAAGCTGGAGCTGAAA 321
         |||||||||||||||||||||
Db   301 GGGACCAAGCTGGAGCTGAAA 321
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RESULT 3
US-11-136-527-190
; Sequence 190, Application US/11136527
; Publication No. US2005028757OA1
; GENERAL INFORMATION:
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William M
;   TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;   FILE REFERENCE: 031896-041000 (AM101086)
;   CURRENT APPLICATION NUMBER: US/11/136,527
;   CURRENT FILING DATE: 2005-05-25
;   PRIOR APPLICATION NUMBER: US 60/574,294
;   PRIOR FILING DATE: 2005-05-26
;   NUMBER OF SEQ ID NOS: 362830
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 190
;   LENGTH: 411
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-190

Query Match   74.8%; Score 240.2; DB 14; Length 411;
Best Local Similarity 82.2%; Pred. No. 1.9e-66;
Matches 264; Conservative 18; Mismatches 36; Indels 3; Gaps 1;

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Qy     1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCCATCTCTGGGAGAAAGTGTCACC 60
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Db    85 GACATCCATGTGACACAGTCTCCTGCCTCCGTGTCTGCATCTCCGGAGAAAATTRTCACC 144
Qy    61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
         |||||||||| ||||| |||| :| | |||| :||:||||||| |||||||||||||||
Db   145 ATCACATGCCAGGGCAGCAGGACCATTGGKARTTSGTTATYATGGTATCAGCAGAAACCA 204
Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCGAGATGGGTCCCATCA 180
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Db   205 GGGAAATCTCCTCAGCTCCTGATCTATRGTGCAAACCAKCTTGGCAGATGGGGTCCCATCA 264
Qy   181 AGGTTCAGTGGCAGTGGATCGGCACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Db   265 AGGTTCAGYGGCAGTAGATCTGGCACACAGTATTCTCTTAAGATCTCTTAAGATCAGCTACAGGTT 324
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Qy   301 GGGACCAAGCTGGAGCTGAAA 321
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Db   382 GGSACCAAGCTGGARWTSAAA 402
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RESULT 4
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; Sequence 4286, Application US/11136527
; Publication No. US2005028757OA1
; GENERAL INFORMATION:
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William M
;   TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;   FILE REFERENCE: 031896-041000 (AM101086)
;   CURRENT APPLICATION NUMBER: US/11/136,527
;   CURRENT FILING DATE: 2005-05-25
;   PRIOR APPLICATION NUMBER: US 60/574,294
;   PRIOR FILING DATE: 2005-05-26
;   NUMBER OF SEQ ID NOS: 362830
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4286
;   LENGTH: 411
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-4286

Query Match   74.8%; Score 240.2; DB 14; Length 411;
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Best Local Similarity    82.3%;  Pred. No. 1.9e-66;
Matches  264;  Conservative  18;  Mismatches  36;  Indels  3;  Gaps  1;

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Db     85 GACATCCATGTGACACAGTCTCCTGCTTCTGCCTCCGTCTCCGGAGAATTRTCACC 144

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
          ||||||||||||||||||||||||  :|||||||||| ||:|||||||||||||||||
Db    145 ATCACATGCCCAGGCACAGCCAGGACATTGKARTTSGTTATYATGGTATCAGCAGAAACCA 204

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          ||||||||||||||||||||||||  ||| ||| |||||||||||||||||||||||||
Db    205 GGGAAATCTCCTCAGCTCCTGATCTATRGTGCAACCAKCTTGGCAGATGGGGTCCCATCA 264

Qy    181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
          |||||||| ||||||||:|| |||||||||||||||||||||||||||||||||||:||
Db    265 AGGTTCAGYGGCAGTAGATCTCGGCACACAGTATTCTCTTAAGATCAGCAGACTACRGGTT 324

Qy    241 GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
          |||||| ||| |||| ||||:|:   ||||||  :||||:  |:|||||||||:::
Db    325 GAAGATATTGGAAYCTATTACTGTYCACAGKYTTMRAGTKCTC---TSACGTTCGGTKSW 381

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
          ||:||||||||||||||| :|||
Db    382 GGSACCAAGCTGGGARWTSAAA 402
```

RESULT 5
US-11-128-900-62
; Sequence 62, Application US/11128900
; Publication No. US2005287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 714
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-128-900-62

Query Match   70.6%; Score 226.6; DB 14; Length 714;
Best Local Similarity   81.6%; Pred. No. 5.5e-62;
Matches 262; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCGTCTCTGGGAGAAAGTGTCACC 60
Db     67 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
Db    127 ATCACTTGCCCGGGCAAGTCAGAGCATTAACAGCTATTTAGATTGGTATCAGCAGAAACCA 186

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
```

RESULT 6
US-10-893-483-188/c
; Sequence 188, Application US/10893483
; Publication No. US2006002699A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Platzer, Josef
; APPLICANT: Schooten, Wim van
; TITLE OF INVENTION: Humanized Immunoglobulin Loci
; FILE REFERENCE: 39691-0007A
; CURRENT APPLICATION NUMBER: US/10/893,483
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,733
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 13281
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized light chain locus
US-10-893-483-188

Query Match   70.6%; Score 226.6; DB 9; Length 13281;
Best Local Similarity   81.6%; Pred. No. 2.1e-61;
Matches 262; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

```
Qy      1 GACATTCAGATGACCCAGTCTCCTGCCTCCGTCTCTGGGAGAAAGTGTCACC 60
Db   9439 GACATCCAGATGACCCAGTCTCCTTCCTTCCACCCGTCTGCATCTGTAGGAGACAGAGTCACC 9380

Qy     61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
Db   9379 ATCACTTGCCCGGGCAAGTCAGAGCATTAGTAGCTGGTTGGCCTGGTATCAGCAGAAACCA 9320

Qy    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
Db   9319 GGGAAAGCCCCTAAGCTCCTGATCATCATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCA 9260

Qy    181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
Db   9259 AGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCACCATCAGCAGCCTGCAGCCT 9200

Qy    241 GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
Db   9199 GATGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTATCCTCTCACTTTCGGCGGT 9140

Qy    301 GGGACCAAGCTGGAGCTGAAA 321
Db   9139 GGGACCAAGTGGGATCTCAAA 9119
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RESULT 7
US-11-144-248-54
; Sequence 54, Application US/11144248
; Publication No. US2005024408A1

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Db    187 GGGAAAGCCCCTAAACTCCTGATCTATGCTGCACAAAATTTCTTCAAGATCAGCAGCCTACAGTTTGCAAAGTGGGGTCCCATCA 246
Qy    181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
Db    247 AGGTTCAGTGGCAGTGGATCTGGGAAGAGAATTRTCACCATCAGCAGTCTGCAACCT 306
Qy    241 GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
Db    307 GAAGATTTGCAACTTACTACTGTCAACAGTATTACAGTACTCCATTCACTTTCGGCCCT 366
Qy    301 GGGACCAAGCTGGAGCTGAAA 321
Db    367 GGGACCAAAGTGGAAATCAAA 387
```

; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: sequence
US-11-144-248-54

Query Match   70.0%;   Score 224.6; DB 12; Length 322;
Best Local Similarity   78.5%;   Pred. No. 1.7e-61;
Matches 252; Conservative 12; Mismatches 57; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60
          ||||||||||||||||||||||||||||||| ||||||| : ||||| |||||||||||
Db   1 GACATCCAGATGACCCAGTCTCCATCTCCGTCTGCATCTGYAGGAGACAGAGTCACC   60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACACATGGTTAGCATGTATCAGCAGAAACCA 120
          |||| |||| |||||||||||||||| ||||||| :|: || :||||||||||||||||
Db   61 ATCACTTGCCGGGCAAGTCAGAGCATTAGYASCTWTTAAATTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          |||||| ||| ||||||||||| : ||| |||| : ||||||||||||||||||||||
Db   121 GGGAAAGCCCCTAARCTCCTGATCYATGYTGCCACAAGTGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACCAACAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
          |||||||||||||||||| ||| || : ||||||||||||||| || || |||||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTTCTCCATTCACGTTCGGTGCT 300
          |||||||||||| : |||:| |||||||||| ||| : |: |||||||
Db   241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACARTRCCCCAYYCHCTTTCGGCGGA 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
          ||||||||| |||||| |||
Db   301 GGGACCAAGTGGGAGATCAA 321

RESULT 8
US-11-144-222-54
; Sequence 54, Application US/11144222
; Publication No. US20050281812A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,222
; CURRENT FILING DATE: 2005-06-02
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927

; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: sequence
US-11-144-222-54

Query Match   70.0%;   Score 224.6; DB 14; Length 322;
Best Local Similarity   78.5%;   Pred. No. 1.7e-61;
Matches 252; Conservative 12; Mismatches 57; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60
          ||||||||||||||||||||||||||||||| ||||||| : ||||| |||||||||||
Db   1 GACATCCAGATGACCCAGTCTCCATCTCCGTCTGCATCTGYAGGAGACAGAGTCACC   60

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACACATGGTTAGCATGTATCAGCAGAAACCA 120
          |||| |||| |||||||||||||||| ||||||| :|: || :||||||||||||||||
Db   61 ATCACTTGCCGGGCAAGTCAGAGCATTAGYASCTWTTAAATTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
          |||||| ||| ||||||||||| : ||| |||| : ||||||||||||||||||||||
Db   121 GGGAAAGCCCCTAARCTCCTGATCYATGYTGCCACAAGTGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACCAACAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
          |||||||||||||||||| ||| || : ||||||||||||||| || || |||||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTTCTCCATTCACGTTCGGTGCT 300
          |||||||||||| : |||:| |||||||||| ||| : |: |||||||
Db   241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACARTRCCCCAYYCHCTTTCGGCGGA 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
          ||||||||| |||||| |||
Db   301 GGGACCAAGTGGGAGATCAA 321

RESULT 9
US-11-182-343-54
; Sequence 54, Application US/11182343
; Publication No. US2006018910A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce
; APPLICANT: Gualberto, Antonio
; APPLICANT: Melvin, Carrie
; APPLICANT: Roberts, Luisa M.
; TITLE OF INVENTION: COMBINATION TREATMENT FOR BREAST CANCER
; FILE REFERENCE: PC32226A
; CURRENT APPLICATION NUMBER: US/11/182,343
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 60/588,721
; PRIOR FILING DATE: 2004-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54
; LENGTH: 322
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus Sequence
US-11-182-343-54

Query Match   70.0%;   Score 224.6; DB 14; Length 322;
Best Local Similarity   78.5%;   Pred. No. 1.7e-61;
Matches 252; Conservative 12; Mismatches 57; Indels 0; Gaps 0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCAGTCTGCATCTCTGGGAGAAAGTGTCACC   60
          ||||||||||||||||||||||||||||||| ||||||| : ||||| |||||||||||
Db   1 GACATCCAGATGACCCAGTCTCCATCTCCGTCTGCATCTGYAGGAGACAGAGTCACC   60

US-10-893-483-188
; Sequence 188, Application US/10893483
; Publication No. US20060026696A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Platzer, Josef
; APPLICANT: Schooten, Wim van
; TITLE OF INVENTION: Humanized Immunoglobulin Loci
; FILE REFERENCE: 39691-0007A
; CURRENT APPLICATION NUMBER: US/10/893,483
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,733
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188
;   LENGTH: 13281
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanized light chain locus
US-10-893-483-188

  Query Match   69.1%;   Score 221.8; DB 9;   Length 13281;
  Best Local Similarity   80.7%;   Pred. No. 7.3e-60;
  Matches   259; Conservative   0; Mismatches   62; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCAGTCTGCATCTCGGGAGAAAGTGTCACC 60
            |||||||||||||||||||||||||| ||||||||||| ||| |||||| |||||||
Db 12395 GACATCCAGATGACCCAGTCCCAGTCTCCATCTCCGTCTCTGCATCTGTAGGAGACAGAGTCACC 12454

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACAGTGGTTAGCATGCATGGTATCAGCAGAAACCA 120
            |||||| ||||||||||||||||||||| || |||||||||||||||||||||||||||||||
Db 12455 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCATTTAAATTGGTATCAGCAGAAACCA 12514

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            |||||||||||||||||||||||| ||| ||||||||||||||| ||||||||||||||
Db 12515 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 12574

Qy   181 AGGTTCAGTGGCAGTGGATCTGGGACAGATCAGCAGCCTACAGGCT 240
            |||||||||||||||||||||| | | ||||||||| |||| |||
Db 12575 AGGTTCAGTGGCAGTGGATCTGGGACAGATTAAGTGCTCACACAGGCT 12634

Qy   241 GAAGATTTTGCAACTTACTACTGTCAACAAGTTACAGTGCTCCATTCGGGTCGGTGCT 300
            |||||||||||||||| ||||||| |||| ||||||||||||||| |||||||| |||
Db 12635 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCTCCACTTTCGGCGGA 12694

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
            |||||||||||||||| |||
Db 12695 GGGACCAAGGTGGAGATTAAA 12715

RESULT 12
US-11-199-739-173
; Sequence 173, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; CURRENT. FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
            |||||| ||||||||||||||||||:| | |||||||||||||||||||||
Db   61 ATCACTTGCCGGGCAAGTCAGAGCATTAGYASCTWTTTAAATTGGTATCAGCAGAAACCA 120

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            |||||| ||| |:|||||| ||| ::|:||| ||: : ||||||||||||||
Db   121 GGGAAAGCCCCTAAARCTCCTGATCYATGYTGCATCCAGTTTRCAARGTGGGGTCCCATCA 180

Qy   181 AGGTTCAGTGGCAGTGGATCTGGGACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
            ||||||||||||||||| || ||| |||||||||| | |||||||||| |||||||
Db   181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCCACCATCAGCAGTGTCTGCAACCT 240

Qy   241 GAAGATTTTGTGAAATTATTACTGTCAACAAGTTTACAGTTTACAGTGCTCCATTCGGGTCGGTGCT 300
            ||||||||| ||| |||||||| ||||||||| :|:| |||||||||||:|:| ||||||:||||||
Db   241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAARTRCCCCAYYCHCTTTCGGCGGA 300

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
            |||||||||||||| | |||
Db   301 GGGACCAAGGTGGAGATCAAA 321

RESULT 10
US-11-086-289-7
; Sequence 7, Application US/11086289
; Publication No. US20060002929A1
; GENERAL INFORMATION:
; APPLICANT: KHARE, SANJAY D.
; APPLICANT: KELLERMANN, SIRID-AIMEE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; FILE REFERENCE: 06843.0094-00000
; CURRENT APPLICATION NUMBER: US/11/086,289
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/555,396
; PRIOR FILING DATE: 2004-03-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
;   LENGTH: 708
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-086-289-7

  Query Match   69.1%;   Score 221.8; DB 14; Length 708;
  Best Local Similarity   80.7%;   Pred. No. 1.9e-60;
  Matches   259; Conservative   0; Mismatches   62; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
            |||||||||||||||||||||| ||||||||||||||||||| ||| |||||| ||||||
Db   67 GACATCCAGATGACCCAGTCCCAGTCTCCCTGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGCATGGTATCAGCAGAAACCA 120
            |||||| ||||||||||||||||||| | | |||||||||||||||||||||||
Db   127 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 186

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
            |||||| |||||||||||| ||| ||| ||||||||||||||| ||||||||||||||
Db   187 GGGAAAGCCCCTAAGCTCCTGATCTTTGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246

Qy   181 AGGTTCAGTGGCAGTGGATCTGGGACAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT 240
            ||||||||||||||||| ||| ||| ||||||||| | |||||||||| |||||||
Db   247 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCCACCATCAGCAGTCTGCAACCT 306

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
            ||||||||| | |||||||| ||||||||| ||||||| ||:| ||||| ||||||||
Db   307 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCATTCACTTTCGGCCCT 366

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
            |||||||||||||| | |||
Db   367 GGGACCAAGGTGGAGATATCAA 387

RESULT 11

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 173
;  LENGTH: 324
;  TYPE: DNA
;  ORGANISM: ARTIFICIAL
;  FEATURE:
;  OTHER INFORMATION: Antibody
US-11-199-739-173

Query Match             68.6%;    Score 220.2; DB 11; Length 324;
Best Local Similarity   80.4%;    Pred. No. 4.3e-60;
Matches   258;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy        1  GACATTCAGATGACGACCCAGTCTCCTGCCTCCAGTCGCATCTCTGGGAGAAAGTGTCACC  60
                  |||||||||| ||||||| ||||||||||||||||||||||| |||||||||
Db        4  GACATCCAGATGACGACCCAGTCTCCAGTCCCTGTCTGCATCCTCTGTAGGAGACAGAGTCACC  63

Qy       61  ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAACCA  120
                  |||||||||||||| ||||  ||||||  ||||||||||||||||||||||||||||||
Db       64  ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA  123

Qy      121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
                  |||||||     |||||||| |||| |||||  ||||||||||||||  ||||||||||
Db      124  GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA  183

Qy      181  AGGTTCAGTGGCAGTGGATCTGGCACAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT  240
                  |||||||||||||||||||||||||  |||| ||||||||||||| |||| ||||||||
Db      184  AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT  243

Qy      241  GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTACAGTTCCATTCACGTTCGGTGCT  300
                  |||||||||| ||||  ||||||||||  |||||| ||| |||  ||||||||||||||
Db      244  GAAGATTTTGCAACTTACTATTGTCAACAGAGTTACAGTACCCCTCCCACTTTCGGCGGA  303

Qy      301  GGGACCAAGCTGGAGCTGAAA  321
                  |||||||| |||||  | |||
Db      304  GGGACCAAGTGGAGATCAAA  324


RESULT 13
US-11-049-536-173
;  Sequence 173, Application US/11049536
;  Publication No. US2006024297A1
;  GENERAL INFORMATION:
;  APPLICANT: Wood, Clive R.
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT: Pieters, Henk
;  APPLICANT: Hoet, Rene
;  APPLICANT: Hufton, Simon E.
;  TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
;  FILE REFERENCE: 10280-128001
;  CURRENT APPLICATION NUMBER: US/11/049,536
;  CURRENT FILING DATE: 2005-02-02
;  PRIOR APPLICATION NUMBER: US 10/916,840
;  PRIOR FILING DATE: 2004-08-12
;  PRIOR APPLICATION NUMBER: US 60/494,713
;  PRIOR FILING DATE: 2003-08-12
;  NUMBER OF SEQ ID NOS: 721
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 173
;  LENGTH: 324
;  TYPE: DNA
;  ORGANISM: ARTIFICIAL SEQUENCE
;  FEATURE:
;  OTHER INFORMATION: Antibody
US-11-049-536-173

Query Match             68.6%;    Score 220.2; DB 14; Length 324;
Best Local Similarity   80.4%;    Pred. No. 4.3e-60;
Matches   258;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy        1  GACATTCAGATGACGACCCAGTCTCCTGCCTCCAGTCGCATCTCTGGGAGAAAGTGTCACC  60
                  |||||||||| ||||||| ||||||||||||||||||||||| |||||||||
Db        4  GACATCCAGATGACGACCCAGTCTCCAGTCCCTGTCTGCATCCTCTGTAGGAGACAGAGTCACC  63
```

```
Qy       61  ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAACCA  120
                  |||||||||||||| ||||  ||||||  |||||||||||||||||||||||||||||
Db       64  ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA  123

Qy      121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
                  |||||||     |||||||| |||| |||||  |||||||||||| |||||||||||||
Db      124  GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA  183

Qy      181  AGGTTCAGTGGCAGTGGATCTGGCACAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT  240
                  |||||||||||||||||||||||||  |||| |||||||||||||| |||| ||||||||
Db      184  AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT  243

Qy      241  GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTACAGTTCCATTCACGTTCGGTGCT  300
                  ||||||||| |||| |||||||||||  |||||| |||  ||||||||||||||||||||
Db      244  GAAGATTTTGCAACTTACTATTGTCAACAGAGTTACAGTACCCCTCCCACTTTCGGCGGA  303

Qy      301  GGGACCAAGCTGGAGCTGAAA  321
                  |||||||| |||||  | |||
Db      304  GGGACCAAGTGGAGATCAAA  324


RESULT 14
US-10-956-008-75
;  Sequence 75, Application US/10956008
;  Publication No. US2006062783A1
;  GENERAL INFORMATION:
;  APPLICANT: Roskos, Lorin
;  APPLICANT: Foltz, Ian
;  APPLICANT: King, Chadwick
;  APPLICANT: Bell, Gregory
;  TITLE OF INVENTION: ANTIBODIES AGAINST PARATHYROID HORMONE
;  FILE REFERENCE: ABGENIX.092CP1
;  CURRENT APPLICATION NUMBER: US/10/956,008
;  CURRENT FILING DATE: 2004-09-30
;  PRIOR APPLICATION NUMBER: 10/638,265
;  PRIOR FILING DATE: 2003-08-08
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 75
;  LENGTH: 322
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-956-008-75

Query Match             68.1%;    Score 218.6; DB 7; Length 322;
Best Local Similarity   80.1%;    Pred. No. 1.4e-59;
Matches   257;  Conservative    0;  Mismatches   64;  Indels    0;  Gaps    0;

Qy        1  GACATTCAGATGACCCAGTCTCCTGCCTCCAGTCTGCATCTGTGGGAGAAAGTGTCACC  60
                  ||||||||||| ||||||||||||||||||||||||||||||| |||||||||||||
Db        1  GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC  60

Qy       61  ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGTATCAGCAGAAACCA  120
                  ||||| |||  ||||||||||||| ||||||  ||||| |||| |||||||||||||||
Db       61  ATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA  120

Qy      121  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA  180
                  ||||||     ||||| ||||||||| ||||| |||||| |||| |||||||||||||||
Db      121  GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCATTTTACAAAGTGGGGTCCCATCA  180

Qy      181  AGGTTCAGTGGCAGTGGATCTGGGACACAAAAATTTCTTTCAAGATCAGCAGCCTACAGGCT  240
                  ||||||||||||||||||||||||||  |||| ||||||||| ||||| |||| |||||||
Db      181  AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT  240

Qy      241  GAAGATTTTGTAAATTATTATTACTGTCAACAAGTTACAGTTCCATTCACGTTCGGTGCT  300
                  |||||||| |||| |||||||||||  |||||||||  ||||  ||||||||||||||||
Db      241  GAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCATTCACTTTCGGCCCT  300

Qy      301  GGGACCAAGCTGGAGCTGAAA  321
                  |||||||| ||||| | ||||
Db      301  GGGACCAAAGTGGATATCAAA  321
```

RESULT 15
US-11-199-739-241
; Sequence 241, Application US/11199739
; Publication No. US20060057138A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Pieters, Henk
; APPLICANT: Hoet, Rene
; APPLICANT: Hufton, Simon E.
; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-135001
; CURRENT APPLICATION NUMBER: US/11/199,739
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: US 11/049,536
; PRIOR FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 10/916,840
; PRIOR FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 726
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 241
; LENGTH: 324
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Antibody
US-11-199-739-241

Query Match   68.1%; Score 218.6; DB 11; Length 324;
Best Local Similarity   80.1%; Pred. No. 1.4e-59;
Matches 257; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

Qy   1 GACATTCAGATGACCCAGTCTCCTGCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
           ||||| ||||||||||||||||||||| ||||||||||||||| | ||||| || |||||
Db   4 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGTAGGAGACAGAGTCACC 63

Qy   61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGCAGAAACCA 120
           ||||| ||||||||||||||||||| ||||| ||||||||||||||||||
Db   64 ATCACTTGCCGGGCAAGTCAGGGCATTAGGCGCATTAGAAATGATTAGGCTGGTATCAGCAGAAAACCA 123

Qy   121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
           |||||| ||| |||||||| |||||||| ||| || |||||||||||||||||||
Db   124 GGGAAAGCCCCTAAGCTCCTGATCTCATGCTGCATCTCCAGTTACAAAGTGGGGTCCCATCA 183

Qy   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTCTTCAAGATCAGCAGCCTACAGGCT 240
           |||||| |||||||||||||||||||||| | || ||| |||||||||| ||| ||
Db   184 AGGTTCAGCGGCAGTGGATCTGGCACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 243

Qy   241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTACAGTTCTCCATTCACGTTCGGTGCT 300
           |||||||||| ||||| |||| |||||||||||||||||| ||||||||||||||||
Db   244 GAAGATTTTGCAACTTATTACTGTCTACACAGATTACAATTACCCGTGGACGTTCGGCCAA 303

Qy   301 GGGACCAAGCTGGAGCTGAAA 321
           ||||||||| | ||| | |||
Db   304 GGGACCAATGTGGAAATCAAA 324

Search completed: April 18, 2006, 18:53:48
Job time : 1341 secs

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OM protein - protein search, using sw model

```
                    GenCore version 5.1.7
          Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on:      April 18, 2006, 13:32:40 ; Search time 230 Seconds
                                      (without alignments)
                                      358.899 Million cell updates/sec

Title:       US-10-764-140-4
Perfect score:  617
Sequence:    1 EIQLQQSGPELVKPGASVQV.........RDVTTALDFWGQGTTLTVSS 117

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:    2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:      2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
        ,    1: uniprot_sprot:*
        ,    2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	476.5	77.2	481	2	Q8VCV5_MOUSE	Q8vcv5 mus musculu
2	475	76.8	117	2	Q9QXF0_MOUSE	Q9qxf0 mus musculu
3	474	76.8	117	2	Q9QXE9_MOUSE	Q9qxe9 mus musculu
4	470	76.2	134	2	Q65ZR6_MOUSE	Q65zr6 mus musculu
5	470	76.2	483	2	Q4VAB6_MOUSE	Q4vab6 mus musculu
6	463	75.0	117	1	HV12_MOUSE	P01756 mus musculu
7	460	74.6	117	1	HV13_MOUSE	P01757 mus musculu
8	447	72.4	470	2	Q7TMK1_MOUSE	Q7tmk1 mus musculu
9	442.5	71.7	488	2	Q91WR1_MOUSE	Q91wr1 mus musculu
10	442	71.6	472	2	Q6PJA7_MOUSE	Q6pja7 mus musculu
11	439	71.2	123	2	Q8VIJ1_MOUSE	Q8vij1 mus musculu
12	433.5	70.3	118	1	HV51_MOUSE	P06310 mus musculu
13	425	68.9	120	2	Q920E8_MOUSE	Q920e8 mus musculu
14	420.5	68.2	485	2	Q58E61_MOUSE	Q58e61 mus musculu
15	420	68.1	458	2	Q5BJZ2_RAT	Q5bjz2 rattus norv
16	419	67.9	117	1	HV14_MOUSE	P01758 mus musculu
17	418	67.7	136	1	HV15_MOUSE	P01759 mus musculu
18	414	67.1	120	1	HV03_MOUSE	P01747 mus musculu
19	412	66.8	477	2	Q58E56_MOUSE	Q58e56 mus musculu
20	411	66.6	481	2	Q91WT1_MOUSE	Q91wt1 mus musculu
21	410	66.5	142	2	Q924Q1_MOUSE	Q924q1 mus musculu
22	408	66.1	170	2	Q92SS2_MOUSE	Q92ss2 mus musculu
23	407.5	66.0	145	2	Q924Q9_MOUSE	Q924q9 mus musculu
24	404.5	65.6	143	2	Q924R0_MOUSE	Q924r0 mus musculu
25	404.5	65.6	145	2	Q924R4_MOUSE	Q924r4 mus musculu
26	402.5	65.2	145	2	Q924Q6_MOUSE	Q924q6 mus musculu
27	402	65.2	146	2	Q924Q8_MOUSE	Q924q8 mus musculu
28	401.5	65.1	141	2	Q924Q4_MOUSE	Q924q4 mus musculu
29	400.5	64.9	137	2	Q924R6_MOUSE	Q924r6 mus musculu
30	400	64.8	140	1	HV02_MOUSE	P01746 mus musculu
31	400	64.8	146	2	Q924Q3_MOUSE	Q924q3 mus musculu
32	399.5	64.7	243	2	Q7TQM2_MOUSE	Q7tqm2 mus musculu
33	399.5	64.7	465	2	Q6PJB2_MOUSE	Q6pjb2 mus musculu
34	399	64.7	146	2	Q924R8_MOUSE	Q924r8 mus musculu
35	398.5	64.6	139	1	HV07_MOUSE	P01751 mus musculu
36	398.5	64.6	145	2	Q924Q7_MOUSE	Q924q7 mus musculu
37	398.5	64.6	590	2	Q4V9V8_MOUSE	Q4v9v8 mus musculu
38	398	64.6	617	2	Q4KML5_MOUSE	Q4km15 mus musculu
39	398	64.4	468	2	Q569W9_MOUSE	Q569w9 mus musculu
40	397.5	64.4	145	2	Q924R1_MOUSE	Q924r1 mus musculu
41	397	64.3	458	2	Q5BK05_RAT	Q5bk05 rattus norv
42	396.5	64.3	482	2	Q8K172_MOUSE	Q8k172 mus musculu
43	395.5	64.1	109	2	Q9JL75_MOUSE	Q9jl75 mus musculu
44	394.5	63.9	143	2	Q924P9_MOUSE	Q924p9 mus musculu
45	394	63.9	140	2	Q924P8_MOUSE	Q924p8 mus musculu

ALIGNMENTS

```
RESULT 1
Q8VCV5_MOUSE
ID   Q8VCV5_MOUSE PRELIMINARY;      PRT;   481 AA.
AC   Q8VCV5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   LOC238447 protein.
GN   Name=LOC238447;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mix FVB/N;
RC   TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mix FVB/N;
RC   TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RG   NIH MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018455; AAH18455.1; -; mRNA.
DR   HSSP; P01810; 2FBJ.
DR   SMR; Q8VCV5; 20-239.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_cl.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
```

```
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   481 AA;  52326 MW;  52B44C5826807143 CRC64;

Query Match             77.2%;  Score 476.5;  DB 2;  Length 481;
Best Local Similarity   75.4%;  Pred. No. 4.1e-39;
Matches   89;  Conservative  13;  Mismatches  15;  Indels   1;  Gaps   1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              |||||||||||||||||||:||| |:||||| :||||||||||||||||||||||||| :||
Db         20 EIQLQQSGPELVRPGTSVKVSCKASGYSFIDYNIYWVKQSHGKSLEWIGYIDPYNGGSSY 79

Qy         61 DQNFKGKATLTVDKSSSTAFMHLNSLTSDDSAVYFCARDVTTA-LDFWGQGTTLTVSS 117
              :|:|||||||||||||| |||:||:|| :|:|:|||| : |||||   ||||||:||||
Db         80 NQKFKGKATLTVDKSSNTAFMYLNNLTSEDSAFYYCAREWYGAWFAFWGQGTLVTVSA 137
```

RESULT 2
```
Q9QXF0_MOUSE
ID   Q9QXF0_MOUSE PRELIMINARY;      PRT;   117 AA.
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Immunoglobulin heavy chain V-D-J region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA   Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
RT   "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT   selective B cell stimulation in (NZB x NZW)F1 mice.";
RL   J. Exp. Med. 176:761-779(1992).
DR   EMBL; AJ225171; CAB65236.1; -; mRNA.
DR   PIR; PH0973; PH0973.
DR   HSSP; Q9QXF0; 1NQB.
DR   SMR; Q9QXF0; 1-117.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1      1
FT   NON_TER      117    117
SQ   SEQUENCE   117 AA;  13060 MW;  DB16AD0858A47E4C CRC64;

Query Match             77.0%;  Score 475;  DB 2;  Length 117;
Best Local Similarity   76.1%;  Pred. No. 1.2e-39;
Matches   89;  Conservative  13;  Mismatches  15;  Indels   0;  Gaps   0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              |||||||||||||||||||:||| |:||||||:|||||||||||||||||:|:| |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 DQNFKGKATLTVDKSSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              :|:||||||||||||||| |||:|| :|:|::|:|||| : ||:|:||||||:||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYAMDYWGQGTSVTVSS 117
```

RESULT 3
```
Q9QXE9_MOUSE
ID   Q9QXE9_MOUSE PRELIMINARY;      PRT;   117 AA.
AC   Q9QXE9;
```

```
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoglobulin heavy chain V-D-J region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2499887;
RA   Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT   "Two murine natural polyreactive autoantibodies are encoded by
RT   nonmutated germ-line genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR   EMBL; AJ225174; CAB65237.1; -; mRNA.
DR   PIR; F33932; F33932.
DR   HSSP; P01751; 1NQB.
DR   SMR; Q9QXE9; 1-117.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER        1      1
FT   NON_TER      117    117
SQ   SEQUENCE   117 AA;  13000 MW;  CDDE2AF84D499734 CRC64;

Query Match             76.8%;  Score 474;  DB 2;  Length 117;
Best Local Similarity   75.2%;  Pred. No. 1.5e-39;
Matches   88;  Conservative  16;  Mismatches  13;  Indels   0;  Gaps   0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
              :|||||||||||||||||||:||| |:||||||:|||||||||||||||||:|:|  |
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 DQNFKGKATLTVDKSSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              :|:||||||||||||||| |||:||:|| :|:|::|:|||| : ||:|:|||||:||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYAMDWGQGTSVTVSS 117
```

RESULT 4
```
Q65ZR6_MOUSE
ID   Q65ZR6_MOUSE PRELIMINARY;      PRT;   134 AA.
AC   Q65ZR6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Ab 126.33 heavy chain variable and joining regions (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91237115; PubMed=1709665;
RA   Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
RT   "Junctional diversity of H and L chains allows the coexpression of two
RT   mutually exclusive idiotopes (IdI104 and IdI558).";
RL   J. Immunol. 146:4024-4030(1991).
DR   EMBL; M74139; AAA37776.1; -; mRNA.
DR   SMR; Q65ZR6; 18-134.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
```

```
FT   NON_TER         1      1
SQ   SEQUENCE      134 AA;  14908 MW;  1852D86D26FC7567 CRC64;

Query Match             76.2%;  Score 470;  DB 2;  Length 134;
Best Local Similarity   75.2%;  Pred. No. 4.4e-39;
Matches     88;  Conservative     14;  Mismatches     15;  Indels      0;  Gaps      0;

Qy      1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
            : |||||||||||||||||||::||  ||:||||   || :|| ||||||| |:|:|||
Db     18 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWVKQSPGKSLEWIGDINPNNGGTSY 77

Qy     61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
            :||||||||||||||||||||||| ||||||||||||||   :: :|||||||||||
Db     78 NQKFKGKATLTVDKSSTAYMQLNSLTSEDSAVYYCARDYSVVFDYWGQGTTLTVSS 134


RESULT 5
ID   Q4VAB6_MOUSE
AC   Q4VAB6;
Q4VAB6_MOUSE PRELIMINARY;    PRT;   483 AA.
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC096462; AAH96462.1; -; mRNA.
KW   Hypothetical protein.
SQ   SEQUENCE    483 AA;  52436 MW;  368E7BEE6B6DE9EF CRC64;

Query Match             76.2%;  Score 470;  DB 2;  Length 483;
Best Local Similarity   76.5%;  Pred. No. 1.8e-38;
Matches     91;  Conservative     12;  Mismatches     14;  Indels      2;  Gaps      2;

Qy      1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
            : |||||||||||||||||||::||  ||:||||   || :|| ||||||| |:|:|||
Db     20 EIQLHQSGPELVKPGTSVKMSCKASGYTFNYNMHWVRQSHGKSLEWIGYIYPNSGATSY 79

Qy     61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTAL-DFWGQGTTLTVSS 117
            :||||||||||||||||||||||  ||||||||||||| :: ||| |:|||||||||||
Db     80 NQKFKGKATLTVDKSSTAYMELRSLTSDDSAVYYCARGDLRTGLFDYWGQGTTLTVSS 138
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RESULT 6
ID   HV12_MOUSE        STANDARD;      PRT;   117 AA.
AC   P01756;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region MOPC 104E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RX   MEDLINE=83075344; PubMed=6816276;
RA   Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA   Hood L.E.;
RT   "Complete amino acid sequence of a mouse mu chain: homology among
RT   heavy chain constant region domains.";
RL   Biochemistry 21:5415-5424(1982).
CC   -!- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma
CC       protein has also been determined.
CC   -!- MISCELLANEOUS: This protein binds dextran.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   PIR; A02039; MHMS4E.
DR   HSSP; P01751; 1NQB.
DR   SMR; P01756; 1-117.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    116       Ig-like.
FT   CARBOHYD     55     55       N-linked (GlcNAc...) (complex).
FT   DISULFID     22     96       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE    117 AA;  12983 MW;  3CF8ACE4B447E41 CRC64;

Query Match             75.0%;  Score 463;  DB 1;  Length 117;
Best Local Similarity   74.4%;  Pred. No. 1.9e-38;
Matches     87;  Conservative     13;  Mismatches     17;  Indels      0;  Gaps      0;

Qy      1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
            : |||||||||||||||||||::||  ||:||||   || :|| ||||||| |:|:|||
Db      1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy     61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
            :||||||||||||||||||||||| ||||||||||||||   |||||||||||||||
Db     61 NQKFKGKATLTVDKSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTTVTVSS 117


RESULT 7
ID   HV13_MOUSE        STANDARD;      PRT;   117 AA.
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: The sequences of 10 hybridoma proteins that also
CC       bind dextran differ from that shown at 1-7 positions, many of
CC       which occur in the D and J segments.
CC   -!- MISCELLANEOUS: This protein binds dextran.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A26242; MHMSJ5.
DR   HSSP; P01751; 1NQB.
DR   SMR; P01757; 1-117.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    116       Ig-like.
FT   DISULFID     22     96       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13025 MW;  292E2AF4BE447E41 CRC64;

Query Match             74.6%;  Score 460;  DB 1;  Length 117;
Best Local Similarity   74.4%;  Pred. No. 3.8e-38;
Matches   87;  Conservative   13;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
              |:||||||||||||||||| :||| ||:|||| : ||:||||||||||| :| ||||
Db          1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy         61 DQNFKGKATLTVDKSSSTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
              :|||||||||||||||||||:|:|||||:||:|||||||||:| |||||||||||||
Db         61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWYFDVWGAGTTVTVSS 117

RESULT 8
Q7TMK1_MOUSE
ID   Q7TMK1_MOUSE PRELIMINARY;    PRT;   470 AA.
AC   Q7TMK1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein AI324046.
GN   Name=AI324046;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II.
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC055910; AAH55910.1; -; mRNA.
DR   HSSP; P01865; 1KB5.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   InterPro; IPR003597; Ig_C1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   470 AA;  51728 MW;  6D90E4DF896BB090 CRC64;

Query Match             72.4%;  Score 447;  DB 2;  Length 470;
Best Local Similarity   69.4%;  Pred. No. 3.6e-36;
Matches   84;  Conservative   16;  Mismatches   17;  Indels    4;  Gaps    1;

Qy          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
              |:||||||||||||||| ||:|| :||||||:: ::||||||||||| :| ||||||
Db         20 EVQLQQSGPELVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSY 79

Qy         61 DQNFKGKATLTVDKSSSTAFMHLNSLTSDDSAVYFCARDVTTA---LDFWGQGTTLTVS 116
              :||||||||||||||||||:||:||||||:||:|||||||:||    |||||||||||||
Db         80 NQKFKGKATLTVDKSSSTAYMELNSLTSEDSAVYYCARYYYSGSYWYFDVWGAGTTVTVS 139

Qy        117 S 117
              |
Db        140 S 140

RESULT 9
Q91WR1_MOUSE
ID   Q91WR1_MOUSE PRELIMINARY;    PRT;   488 AA.
AC   Q91WR1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Igh-VJ558 protein.
GN   Name=Igh-VJ558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013539; AAH13539.1; -; mRNA.
DR   HSSP; P01751; 1A6W.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   MGI; MGI:96486; Igh-VJ558.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   488 AA;   52965 MW;  F12068460B400B9D CRC64;

Query Match             71.7%;  Score 442.5;  DB 2;  Length 488;
Best Local Similarity   68.5%;
Matches   85;  Conservative   14;  Mismatches   18;  Indels    7;  Gaps    1;

Qy    1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
         |:|||||||||||||||||||:||  ||: |||:||||||||||||||||:||||||
Db   20 EVQLQQSGPELVKPGASVKLSCKASGYTITDYYVNWVKQSHGKSLEWIGDINPYNGGTSY 79

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVT------TALDFWGQGTTL 113
         :| |||||||||||:|:|||||||||||||||||||: ||      :||||||||||
Db   80 NQKFKGKATLTVDKSSSIAYMQLNNLTSDDSAVYYCARGPVYYSYFSYDRGDYWGQGTLV 139

Qy  114 TVSS 117
          ||:
Db  140 TVSA 143

RESULT 10
Q6PJA7_MOUSE
ID   Q6PJA7_MOUSE PRELIMINARY;    PRT;   472 AA.
AC   Q6PJA7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   Name=Igh-1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Czech II;
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```
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018535; AAH18535.1; -; mRNA.
DR   HSSP; P01865; 1KB5.
DR   MGI; MGI:96443; Igh-1a.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig-.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IGc1; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;   52299 MW;  165169C23D55D4AB CRC64;

Query Match             71.6%;  Score 442;  DB 2;  Length 472;
Best Local Similarity   68.3%;     Pred. No. 1.1e-35;
Matches   84;  Conservative   16;  Mismatches   17;  Indels    6;  Gaps    1;

Qy    1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
         |:|||||||||||||||||||:||  ||: |||:||||||||||||||||:||||||
Db   20 EVQLQQSGPELVKTGASVKMSCKASGYTFSDYYMHWVKQSHGKSLEWIGYIYPNNGGNGY 79

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTT------ALDFWGQGTLT 114
         :| |||||||||||:|:|||||||||||:|||||||||:||      :||||||||||
Db   80 NQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARGYISYSYDHYFDYWGQGTTIT 139

Qy  115 VSS 117
         |||
Db  140 VSS 142

RESULT 11
Q8VIJ1_MOUSE
ID   Q8VIJ1_MOUSE PRELIMINARY;    PRT;   123 AA.
AC   Q8VIJ1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-DNA heavy chain (Fragment).
```

GN　Name=J558;
OS　Mus musculus (Mouse).
OC　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC　Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC　Muridae; Murinae; Mus.
OX　NCBI_TaxID=10090;
RN　[1]
RP　NUCLEOTIDE SEQUENCE.
RC　STRAIN=C3H/HeJ-lpr/lpr;
RX　MEDLINE=9409289; PubMed=8814271;
RA　Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT　"Differences in V kappa gene utilization and VH CDR3 sequence among
RT　anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL　Eur. J. Immunol. 26:2225-2233(1996).
DR　EMBL; U59154; AAB02916.1; -; mRNA.
DR　HSSP; P01751; 1NQB.
DR　SMR; Q8VIJ1; 1-123.
DR　Ensembl; ENSMUSG00000057521; Mus musculus.
DR　InterPro; IPR007110; Ig-like.
DR　InterPro; IPR003596; Ig_v.
DR　SMART; SM00406; IGv; 1.
DR　PROSITE; PS50835; IG_LIKE; 1.
FT　NON_TER　　1　1
FT　NON_TER　123　123
SQ　SEQUENCE　123 AA;　13806 MW;　CC0037A806E9911E CRC64;

Query Match　　　　71.2%;　Score 439;　DB 2;　Length 123;
Best Local Similarity　69.1%;　Pred. No. 5.1e-36;
Matches　85;　Conservative　12;　Mismatches　20;　Indels　6;　Gaps　1;

Qy　　1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
　　　　||||||||||||||||||| ||||||::||||| ||||:|:|||||||
Db　　1 EIQLQQSGTELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGDINPYYGGTRY 60

Qy　61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVT------TALDFWGQGTTLT 114
　　　　:||||||||||:||||| ||::|||::||||:
Db　61 SQKFKDKATLTVDKSSRTAYMQLNSLTSEDSAVYYCARDYTYYTYDEGCFAYWGQGTLVT 120

Qy　115 VSS 117
　　　　 ||:
Db　121 VSA 123

RESULT 12
HV51_MOUSE
ID　HV51_MOUSE　　　STANDARD;　　　PRT;　118 AA.
AC　P06330;
DT　01-JAN-1988 (Rel. 06, Created)
DT　01-JAN-1988 (Rel. 06, Last sequence update)
DT　10-MAY-2005 (Rel. 47, Last annotation update)
DE　Ig heavy chain V region AC38 205.12.
OS　Mus musculus (Mouse).
OC　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC　Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC　Muroidea; Muridae; Murinae; Mus.
OX　NCBI_TaxID=10090;
RN　[1]
RP　PROTEIN SEQUENCE.
RX　MEDLINE=84182519; PubMed=6201362;
RA　Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT　"A V region determinant (idiotope) expressed at high frequency in B
RT　lymphocytes is encoded by a large set of antibody structural genes.";
RL　EMBO J. 3:517-523(1984).
CC　---
CC　This Swiss-Prot entry is copyright. It is produced through a collaboration
CC　between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC　the European Bioinformatics Institute. There are no restrictions on its
CC　use as long as its content is in no way modified and this statement is not
CC　removed.
CC　---
DR　PIR; A02040; MHMS38.
DR　HSSP; P01751; 1NQB.
DR　SMR; P06330; 1-118.

DR　InterPro; IPR007110; Ig-like.
DR　InterPro; IPR003596; Ig_v.
DR　SMART; SM00406; IGv; 1.
DR　PROSITE; PS50835; IG_LIKE; 1.
KW　Direct protein sequencing; Immunoglobulin domain;
KW　Immunoglobulin V region.
FT　REGION　　　1　　98　　　　　V segment.
FT　REGION　　99　104　　　　　D segment.
FT　REGION　105　118　　　　　J segment.
FT　DISULFID　22　96　　　　　By similarity.
FT　NON_TER　118　118
SQ　SEQUENCE　118 AA;　12934 MW;　94F7BE84C762A018 CRC64;

Query Match　　　　70.3%;　Score 433.5;　DB 1;　Length 118;
Best Local Similarity　70.3%;　Pred. No. 1.7e-35;
Matches　83;　Conservative　13;　Mismatches　21;　Indels　1;　Gaps　1;

Qy　　1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
　　　　|:||||||||||||||||| ||||||::||||| ||||:|:||||||: :|
Db　　1 EVQLQQSGPELVKPGASVKISCKASGYSFTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy　61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDV-TTALDFWGQGTTLTVSS 117
　　　　:|:||||||||||||| ||:|||::||||| ||||||:|:
Db　61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCARGYGYDPFDVWGTGTTVTVSS 118

RESULT 13
Q920E8_MOUSE
ID　Q920E8_MOUSE PRELIMINARY;　　　PRT;　120 AA.
AC　Q920E8;
DT　01-DEC-2001 (TrEMBLrel. 19, Created)
DT　01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT　01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE　Pterin-mimicking anti-idiotope heavy chain variable region
DE　(Fragment).
OS　Mus musculus (Mouse).
OC　Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC　Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC　Muridae; Murinae; Mus.
OX　NCBI_TaxID=10090;
RN　[1]
RP　NUCLEOTIDE SEQUENCE.
RA　Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL　Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR　EMBL; AF307936; AAL09420.1; -; Genomic_DNA.
DR　HSSP; P01751; 1NQB.
DR　SMR; Q920E8; 1-120.
DR　InterPro; IPR007110; Ig-like.
DR　InterPro; IPR003596; Ig_v.
DR　SMART; SM00406; IGv; 1.
DR　PROSITE; PS50835; IG_LIKE; 1.
FT　NON_TER　　1　　1
FT　NON_TER　120　120
SQ　SEQUENCE　120 AA;　13204 MW;　DC4834AB1DE56F3C CRC64;

Query Match　　　　68.9%;　Score 425;　DB 2;　Length 120;
Best Local Similarity　68.3%;　Pred. No. 1.3e-34;
Matches　82;　Conservative　14;　Mismatches　20;　Indels　4;　Gaps　1;

Qy　　1 EIQLQQSGPELVKPGASVQVSCKTKGYSFTDYNVWVRQSHGKSLEWIGYIDPYNGITIY 60
　　　　|:||||||||||||||||| ||||||::||||| ||||:|:|||||||:||||
Db　　1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSNGKSLEWIGNIDPYYGGTSY 60

Qy　61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCA----RDVTTALDFWGQGTTLTVS 116
　　　　:||||||||||||||| ||::|||::|||||　　　　 : :||:||:
Db　61 NQKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCAVIYYGNSPAWFAYWGQGTLVTVS 120

RESULT 14
Q58B61_MOUSE
ID　Q58B61_MOUSE PRELIMINARY;　　　PRT;　485 AA.
AC　Q58B61;
DT　10-MAY-2005 (TrEMBLrel. 30, Created)

DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Igh-VJ558 protein.
GN   Name=Igh-VJ558;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Czech II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC092056; AAH92056.1; -; mRNA.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ   485 AA; 52628 MW; F08C1FB47C4E44EC CRC64;

Query Match   68.2%; Score 420.5; DB 2; Length 485;
Best Local Similarity   65.6%; Pred. No. 1.7e-33; Indels   5; Gaps   1;
Matches 80; Conservative 17; Mismatches 20; Indels 5; Gaps 1;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGVIDPYNGITIY 60
           |:|||||||||| :||||:||||| |:||:||:||||||:||||||| ||||||||||
Db   20 EVQLQQSGAELVKPGASVKISCKASGYTFNDYNMDWVKQSHGRSLEWIGNINPNYDSTIY 79

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVT----TALDFWGQGTTLTV 115
           : ||||||||||:|:||: ||:|:|||||||||:||||| || :|:|| ||||||:|
Db   80 NQKFKGKATLTVEKSSSTAYMELRSLTSDDSAVYYCARTETYYSYDGGFAYWGRGTLVTV 139

Qy   116 SS 117
           |:
Db   140 SA 141

ID   Q5BJZ2_RAT   PRELIMINARY;   PRT;   458 AA.
AC   Q5BJZ2;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   LOC367586 protein.
GN   Name=LOC367586;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC   histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC091272; AAH91272.1; -; mRNA.
DR   SMR; Q5BJZ2; 21-454.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;

Query Match   64.1%; Score 420; DB 2; Length 458;
Best Local Similarity   64.1%; Pred. No. 1.8e-33;
Matches 75; Conservative 20; Mismatches 22; Indels   0; Gaps   0;

Qy   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
           :||||||||:|||||||||||||||:|||||||||||||||||||||||:|||||||||:
Db   20 QVQLQQSGABLVKPGSSVVKISCKASGYTFNYDIHWIKQQPGNGLEWIGWIYPGNGNTKY 79

Qy   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
           : |||||||||:|||:|||||:|||:||||||||||||||:: |||| ||:|||||:
Db   80 NQKFNGKATLTADKSSSTAYMQLSLTSEDSAVFCARDYFPGYDYWGQGVMVTVSS 136

Wed Apr 19 10:36:17 2006

us-10-764-140-4.rup

Search completed: April 18, 2006, 13:39:33
Job time : 231 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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